

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2004, 13:30:29 ; Search time 53 Seconds  
(without alignments)  
836.980 Million cell updates/sec

Title: US-09-716-356A-6  
Perfect score: 812  
Sequence: 1 YFGKLESKSLVIRNLNDQVL.....LXKDELGDRSINFTVQNEED 157

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A. Geneseq\_29Jan04.\*

1: geneseqp1980s.\*  
2: geneseqp1990s.\*  
3: geneseqp2000s.\*  
4: geneseqp2001s.\*  
5: geneseqp2002s.\*  
6: geneseqp2003as.\*  
7: geneseqp2003Bs.\*  
8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	811	99.9	157	2 AAW77077	Human int
2	811	99.9	157	3 AAY57570	Human int
3	811	99.9	157	4 AAG65351	Human int
4	811	99.9	157	4 AAG65294	Human int
5	811	99.9	157	4 AAE06661	Human int
6	811	99.9	157	5 ABB04389	Human int
7	811	99.9	157	5 AAE17134	Human IL-
8	811	99.9	157	5 AAE16954	Human act
9	811	99.9	157	6 ABG73359	Human wil
10	811	99.9	157	6 ADA50616	Human mat
11	811	99.9	157	6 ADA50610	Human mat
12	811	99.9	157	6 ABR83372	Human int
13	811	99.9	157	7 ADE06775	Human int
14	811	99.9	158	3 AAY85167	Human int
15	811	99.9	177	6 ADA50614	Mature co
16	811	99.9	180	2 AAW48959	Wild-type
17	811	99.9	193	2 AAW22047	Interfero
18	811	99.9	193	2 AAW46592	Amino aci
19	811	99.9	193	4 AAB30541	A human I
20	811	99.9	193	3 AAG63830	Amino acl
21	811	99.9	193	5 AAE16953	Human pre
22	811	99.9	233	5 AAE16959	Ubiquitin
23	811	99.9	536	5 AAE16957	Human pro
24	811	99.9	588	5 AAE16958	Human pro
25	811	99.9	1048	5 AAE16960	Ubiquitin

## ALIGNMENTS

RESULT 1

AAW77077

ID AAW77077 standard; peptide; 157 AA.

XX

AC AAW77077;

XX

DT 16-NOV-1998 (first entry)

XX

DE Human interleukin 18.

XX

XX

Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;

KW osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;

KW chronic rheumatoid arthritis; deformity ostitis; primary hyperthyroidism.

XX

OS Homo sapiens.

XX

PN EP861663-A2.

XX

PD 02-SEP-1998.

XX

PF 24-FEB-1998; 98EP-00301352.

XX

PR 25-FEB-1997; 97JP-00055468.

XX

(HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.

XX

Gillespie MT, Horwood NJ, Udagawa N, Kurimoto M;

XX

PI

DR

DR

DR

DR

DR

DR

DR

DR

DR

DR

DR

DR

DR

DR

DR

DR

DR

DR

DR

DR

DR

Best Local Similarity 99.4%; Pred. No. 9.8e-83; Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60	
Db	1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60	
QY	61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNIKOTKSDIIFQRSVPGHDNKMOPESSY 120	
Db	61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNIKOTKSDIIFQRSVPGHDNKMOPESSY 120	
QY	121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157	
Db	121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157	
RESULT 2		
AAI57570	AAI57570 standard; protein; 157 AA.	
ID	AAI57570	
XX	AAI57570;	
AC	06-MAR-2000 (first entry)	
DT	Human interleukin 18 protein sequence SEQ ID NO:1.	
DE	Human; interleukin 18; IL-18; potentiator; IGIF; tumour; cancer;	
KW	interferon-gamma-inducing factor; growth inhibition; cytostatic.	
KW	Human; interleukin 18; IL-18; potentiator; IGIF; tumour; cancer;	
OS	Homo sapiens.	
XX	WO9959565-A1.	
FN	25-NOV-1999.	
XX	20-MAY-1999; 99WO-US011160.	
PD	21-MAY-1998; 98US-0086560P.	
XX	(SMIK ) SMITHKLINE BEECHAM CORP.	
PA	Johnson RK;	
PI	WPI; 2000-062368/05.	
DR	New polypeptides, useful for preparation of composition for preventing	
XX	and/or treating cancer by inhibiting tumor growth.	
PT	Claim 1; Page 49-50; 53pp; English.	
PS	The present sequence represents human interleukin 18 (IL-18). The present	
XX	invention describes a compound comprising human or murine IL-18 in	
CC	combination with a chemotherapeutic agent (I). Also described are: (1) a	
CC	method of preventing and/or treating cancer in a mammal comprising the	
CC	administration of a cancer inhibiting amount of (I) comprising the IL-18	
CC	protein and the chemotherapeutic agent and optionally a pharmaceutically	
CC	acceptable carrier; and (2) a method of inhibiting the growth of tumour	
CC	cells in a mammal sensitive to a composition comprising human IL-18	
CC	and/or murine IL-18 and the chemotherapeutic agent (and optionally a	
CC	pharmaceutically acceptable carrier), comprising administering to a	
CC	mammal afflicted with the tumour cells an effective tumour cell growth	
CC	inhibiting amount of (I). The IL-18 protein in conjunction with a	
CC	chemotherapeutic agent is useful in a method for preventing and/or	
CC	treating cancer in mammals by inhibiting the growth of tumours or	
CC	cancerous cells in mammals	
XX	Sequence 157 AA;	
XX	Query Match 99.9%; Score 811; DB 3; Length 157;	
XX	Best Local Similarity 99.4%; Pred. No. 9.8e-83;	
XX	Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60	
Db	1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60	
QY	61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNIKOTKSDIIFQRSVPGHDNKMOPESSY 120	
Db	61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNIKOTKSDIIFQRSVPGHDNKMOPESSY 120	
QY	121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157	
Db	121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157	
RESULT 3		
AAI65351	AAI65351 standard; protein; 157 AA.	
ID	AAI65351	
XX	AAI65351;	
AC	30-NOV-2001 (first entry)	
DT	Human interleukin-18 (IL-18) protein fragment.	
DE	IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;	
KW	nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;	
KW	immunosuppressive; antidepressant; neuroleptic; hepatotropic.	
OS	Homo sapiens.	
XX	WO200158956-A2.	
FN	16-AUG-2001.	
XX	09-FEB-2001; 2001WO-US004170.	
PD	10-FEB-2000; 2000US-0181608P.	
XX	(BADI ) BASF AG.	
PA	Gayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;	
PI	Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;	
PI	Lennard SN;	
XX	WPI; 2001-550020/61.	
DR	Novel antibodies and compounds capable of binding to human interleukin-18	
XX	useful for treating, e.g., inflammatory disorders, neurological	
PT	disorders, heart failure, myocardial infarction, and autoimmune diseases.	
PT	Disclosure; Page 14; 91pp; English.	
XX	The invention provides isolated antibodies, or antigen-binding portions,	
CC	that are capable of binding to human interleukin-18 (IL-18). The	
CC	antibodies may be used to inhibit human IL-18 activity in, and treat a	
CC	disorder where IL-18 is detrimental in, a human subject suffering from,	
CC	inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,	
CC	inflammatory bowel disease, and osteoarthritis), neurological disorders	
CC	(e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and	
CC	stroke), heart failure, myocardial infarction, autoimmune diseases such	
CC	as autoimmune hepatitis and autoimmune neutropenia, and mental disorders	
CC	(e.g., depression and schizophrenia). Treatment with an anti-IL-18	
CC	antibody may occur before, concurrent, or after administration of a	
CC	second agent selected from an antibody, or fragment, capable of binding	
CC	human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,	
CC	cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory	
CC	agents. The present sequence represents a human IL-18 protein fragment	
XX	Sequence 157 AA;	
XX	Query Match 99.9%; Score 811; DB 4; Length 157;	
XX	Best Local Similarity 99.4%; Pred. No. 9.8e-83;	
XX	Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60	
Db	1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60	

Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNPRTIIFISMYKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKOTKSDIIFORSVPGHNDKNQFESSY 120  
Db 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKOTKSDIIFORSVPGHNDKNQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 4  
AAG65294  
ID AAG65294 standard; protein; 157 AA.  
XX  
AC AAG65294;  
XX  
DT 30-NOV-2001 (first entry)  
XX  
DE Human interleukin-18 (IL-18) protein fragment.  
XX  
KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;  
KW neutrotropic; neurological; antiinflammatory; antiparkinsonian; cardiant;  
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic.  
XX  
OS Homo sapiens.  
XX  
PN WO200158956-A2.  
XX  
PD 16-AUG-2001.  
XX  
PF 09-FEB-2001; 2001WO-US004170.  
XX  
PR 10-FEB-2000; 2000US-0181608P.  
XX  
PA (BADI ) BASF AG.  
XX  
PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;  
PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JB;  
PI Lennard SN;  
XX  
WPI; 2001-550020/61.  
XX  
PT Novel antibodies and compounds capable of binding to human interleukin-18  
PT useful for treating, e.g., inflammatory disorders, neurological  
PT disorders, heart failure, myocardial infarction, and autoimmune diseases.  
XX  
PS Disclosure; Page 9; 91pp; English.  
XX  
CC The invention provides isolated antibodies, or antigen-binding portions,  
CC that are capable of binding to human interleukin-18 (IL-18). The  
CC antibodies may be used to inhibit human IL-18 activity in, and treat a  
CC disorder where IL-18 is detrimental in, a human subject suffering from,  
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,  
CC inflammatory bowel disease, and osteoarthritis), neurological disorders  
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and  
CC stroke), heart failure, myocardial infarction, autoimmune diseases such  
CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders  
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18  
CC antibody may occur before, concurrent, or after administration of a  
CC second agent selected from an antibody, or fragment, capable of binding  
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,  
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory  
CC agents. The present sequence represents a human IL-18 protein fragment  
XX  
SQ Sequence 157 AA;

Query Match 99.9%; Score 811; DB 4; Length 157;  
Best Local Similarity 99.4%; Pred. No. 9.8e-83;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNPRTIIFISMYKDSQPRGM 60

Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNPRTIIFISMYKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKOTKSDIIFORSVPGHNDKNQFESSY 120  
Db 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKOTKSDIIFORSVPGHNDKNQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 5  
AAE06661  
ID AAE06661 standard; protein; 157 AA.  
XX  
AC AAE06661;  
XX  
DT 16-OCT-2001 (first entry)  
XX  
DE Human interleukin-1gamma (IL-1gamma) protein.  
XX  
KW Human; interleukin-1gamma; IL-1gamma; virucide; hepatotropic; fever;  
KW immunological disorder; tumour; inflammatory disorder; hypoglycaemia;  
KW autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;  
KW psoriasis; viral infection; allergy; cytokine; HIV; drug screening.  
XX  
OS Homo sapiens.  
XX  
PN WO200157219-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 01-FEB-2001; 2001WO-US003285.  
XX  
PR 02-FEB-2000; 2000US-0179638P.  
XX  
PA (SCHE ) SCHERING CORP.  
XX  
PI Debets JEMA, Timans JC, Bazan JF, Kastelein RA;  
XX  
WPI; 2001-488886/53.  
XX  
PT Novel isolated or recombinant antigenic interleukin-1 delta or epsilon  
PT polypeptide useful for treating conditions exhibiting abnormal expression  
PT of interleukin such as immunological disorders, tumor and allergy.  
XX  
PS Disclosure; Fig 1; 103pp; English.  
XX  
CC The invention relates to recombinant antigenic interleukin-1 like  
CC molecules and their corresponding nucleic acid sequences, designated as  
CC interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon). IL  
CC -1delta and IL-1epsilon are useful for treating conditions exhibiting  
CC abnormal expression of the interleukin such as immunological disorders,  
CC tumors, inflammatory disorders, fever, hypoglycaemia, psoriasis,  
CC allergy, autoimmune diseases and infectious diseases (e.g., pulmonary  
CC tuberculosis, leprosy, fulminant hepatitis, and viral infections such as  
CC HIV). The invention also relates to methods of using the composition  
CC containing IL-1delta or IL-1epsilon for both diagnostic and therapeutic  
CC utilities. IL-1delta is used as an immunogen for the production of  
CC antisera or antibodies specific, e.g., capable of distinguishing between  
CC IL-1 family members and an IL-1delta, for the interleukin or its  
CC fragment. The purified interleukin is used as a reagent to detect any  
CC antibodies generated in response to the presence of elevated levels of  
CC expression, or immunological disorders which lead to antibody production  
CC to the endogenous cytokine. The invention also contemplates the use of  
CC competitive drug screening assays. The present sequence is human  
CC interleukin-1gamma (IL-1gamma) protein related to the invention  
XX  
SQ Sequence 157 AA;

Query Match 99.9%; Score 811; DB 4; Length 157;  
Best Local Similarity 99.4%; Pred. No. 9.8e-83;



KW Human; interleukin-18; IL-18; caspase; interferon gamma; IFN-gamma;  
KW immunocompetent.

OS Homo sapiens.

PN WO200198455-A2.

PD 27-DEC-2001.

PF 11-JUN-2001; 2001WO-US018804.

PR 15-JUN-2000; 2000US-0211832P.

PR 10-AUG-2000; 2000US-0224128P.

PR 20-JAN-2001; 2001US-0264923P.

PA (SMIK ) SMITHKLINE BEECHAM CORP.

PI Johanson KO, Kirkpatrick RB, Shatzman AR, Hoy YS, Mcdevitt P;

DR WPI; 2002-139786/18.

XX Activation of precursor polypeptide e.g. interleukin-18 polypeptide

PT useful for inducing interferon-gamma production, comprises contacting or

PT co-expressing caspase 4 or caspase 5 with precursor polypeptide.

XX Claim 9; Fig 3; 64pp; English.

XX The invention relates to a method for the in vitro activation of human  
CC precursor interleukin-18 (Pro-IL-18) with an activating enzyme. The  
CC method comprises contacting precursor IL-18 with an activating enzyme  
CC such as caspase 4 or caspase 5. Caspases 4 and 5 are members of a family  
CC of cysteine proteases that include interleukin-1beta converting enzyme  
CC (ICE), which preferentially cleave substrates containing a protease  
CC activation motif. The methods are useful for producing physiologically  
CC active polypeptide e.g. active IL-18 polypeptide. The active IL-18  
CC polypeptide has an activity of inducing the production of interferon  
CC (IFN)-gamma in immunocompetent cells. IFN-gamma is useful as a  
CC biologically active substance for stimulating the production of IFNg from  
CC KG-1 (human myelomonocytic cell line) cells. The present sequence is  
CC human active IL-18 protein

XX Sequence 157 AA;

Query Match 99.9%; Score 811; DB 5; Length 157;  
Best Local Similarity 99.4%; Pred. No. 9.8e-83;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRNPRTFIISMYKDSQPRGM 60

Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRNPRTFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTSKDIIFQSVPGHDKMKQFESSY 120

Db 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTSKDIIFQSVPGHDKMKQFESSY 120

QY 121 EGYFLACEKERDLFKLLKKEDELGRSINFTVQNE 157

Db 121 EGYFLACEKERDLFKLLKKEDELGRSINFTVQNE 157

RESULT 9

ABG73359

ID ABG73359 standard; protein; 157 AA.

XX AC ABG73359;

XX DT 13-MAY-2003 (first entry)

XX Human wild-type mature interleukin-18 (IL-18).

XX Human; human interleukin-18; IL-18; IL-18 binding protein; IL-18BP;  
KW T helper type 1 response; Th1 response; cancer; viral disease;  
KW microbial infection; tumour immunotherapy; adjuvant; DNA vaccination;

KW graft versus tumour therapy; neutralisation; cytostatic; virucide;  
KW antimicrobial.

OS Homo sapiens.

PN US2002169291-A1.

PD 14-NOV-2002.

PF 08-MAR-2002; 2002US-00094153.

PR 08-MAR-2001; 2001US-0274327P.

PA (DINA/) DINARELLO C.

PA (KIMS/) KIM S H.

XX Dinarello C, Kim SH;

DR WPI; 2003-298731/29.

DR N-PSDB; ABX11788.

XX Novel interleukin-18 mutant polypeptide useful in the treatment of cancer

PT and viral disease, has mutations in amino acid residues which are

PT involved in its interaction with IL-18 binding protein.

XX Example 1; Fig 1B; 23pp; English.

XX The present invention relates to mutants of human interleukin-18 (IL-18)  
CC protein that have a lower affinity for IL-18 binding protein (IL-18BP)  
CC than the wild-type IL-18 protein. The IL-18 mutants of the invention  
CC comprise mutations in one or more amino acid residues which are involved  
CC in its interaction with IL-18BP. The mutations comprise substitutions,  
CC preferably non-conservative, additions or deletions. A pharmaceutical  
CC composition comprising an IL-18 mutant is useful for treating a disease  
CC which is prevented or alleviated by a T helper type 1 (Th1) response,  
CC including cancer and viral disease. The IL-18 mutants are useful in the  
CC treatment of the above diseases, microbial infections, in tumour  
CC immunotherapy, and as an adjuvant in DNA vaccination and in graft versus  
CC tumour therapy. The IL-18 mutants are resistant to, or less susceptible  
CC to, neutralisation than the wild-type protein. The present sequence  
CC represents human wild-type mature IL-18 protein

XX Sequence 157 AA;

Query Match 99.9%; Score 811; DB 6; Length 157;  
Best Local Similarity 99.4%; Pred. No. 9.8e-83;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRNPRTFIISMYKDSQPRGM 60

Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRNPRTFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTSKDIIFQSVPGHDKMKQFESSY 120

Db 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTSKDIIFQSVPGHDKMKQFESSY 120

QY 121 EGYFLACEKERDLFKLLKKEDELGRSINFTVQNE 157

Db 121 EGYFLACEKERDLFKLLKKEDELGRSINFTVQNE 157

RESULT 10

ADA50616

ID ADA50616 standard; protein; 157 AA.

XX AC ADA50616;

XX DT 20-NOV-2003 (first entry)

XX Human mature consensus interleukin-18 (IL-18), SEQ ID NO:71.

XX Nucleic acid vaccine; DNA vaccine; tumour antigen; cytokine adjuvant;  
KW humoral response; cellular response; immune response; immunotherapy;

Key	Location/Qualifiers
Misc-difference 4	/note= "Glu may replace wild-type Lys in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"
Misc-difference 5	/note= "Val may replace wild-type Leu in a variant protein. A variant protein with this substitution is unlikely to have changed immunogenicity compared to the wild-type protein"
Misc-difference 6	/note= "Ile may replace wild-type Glu in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"
Misc-difference 8	/note= "Asp may replace wild-type Lys in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"
Misc-difference 10	/note= "Thr may replace wild-type Ser in a variant protein. A variant protein with this substitution would not have changed immunogenicity compared to the wild-type protein"
Misc-difference 12	/note= "Val may replace wild-type Ile in a variant protein. A variant protein with this substitution would not have changed immunogenicity compared to the wild-type protein"
Misc-difference 13	/note= "Ile may replace wild-type Arg in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"
Misc-difference 15	/note= "Arg may replace wild-type Leu in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"
Misc-difference 17	/note= "Lys may replace wild-type Asp in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"
Misc-difference 20	/note= "Val or Ile may replace wild-type Leu in a variant protein. A variant protein with this substitution is unlikely to have changed immunogenicity compared to the wild-type protein"
Misc-difference 21	/note= "Tyr may replace wild-type Phe in a variant protein. A variant protein with this substitution is unlikely to have changed immunogenicity compared to the wild-type protein"
Misc-difference 22	/note= "Val may replace wild-type Ile in a variant protein. A variant protein with this substitution is unlikely to have changed immunogenicity compared to the wild-type protein"
Misc-difference 27	/note= "Lys may replace wild-type Arg in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"
Misc-difference 30	/note= "Ala may replace wild-type Phe in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"
Misc-difference 35	/note= "Lys may replace wild-type Asp in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"
Misc-difference 37	/note= "Phe may replace wild-type Asp in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"

FT protein. A variant protein with this substitution would  
 FT have changed activity compared to the wild-type protein"  
 FT 111  
 FT /note= "Lys may replace wild-type Asn in a variant  
 FT protein. A variant protein with this substitution would  
 FT have changed activity compared to the wild-type protein"  
 FT 129  
 FT /note= "Phe may replace wild-type Lys in a variant  
 FT protein. A variant protein with this substitution would  
 FT have changed activity compared to the wild-type protein"  
 FT 131  
 FT /note= "Asp may replace wild-type Arg in a variant  
 FT protein. A variant protein with this substitution would  
 FT have changed activity compared to the wild-type protein"  
 FT 132  
 FT /note= "Leu may replace wild-type Asp in a variant  
 FT protein. A variant protein with this substitution would  
 FT have changed activity compared to the wild-type protein"  
 FT 133  
 FT /note= "Glu may replace wild-type Leu in a variant  
 FT protein. A variant protein with this substitution would  
 FT have changed activity compared to the wild-type protein"  
 FT 134  
 FT /note= "Ala may replace wild-type Phe in a variant  
 FT protein. A variant protein with this substitution would  
 FT have changed activity compared to the wild-type protein"  
 FT 135  
 FT WO2003031569-A2.  
 FT  
 FT 17-APR-2003.  
 FT  
 FT 18-SEP-2002; 2002WO-US029640.  
 FT  
 FT 10-OCT-2001; 2001US-0328371P.  
 FT  
 FT (CENZ ) CENTOCOR INC.  
 FT  
 FT Snyder L, Scallion B, Knight DM, McCarthy SG, Goletz TJ;  
 FT Branigan PJ;  
 FT WPI: 2003-393437/37.  
 FT N-PSDB; ADA50613.  
 FT  
 FT New nucleic acid vaccine, useful for eliciting an immune response to a  
 FT cancer associated tumor protein in a mammal.  
 FT  
 FT Claim 1b; Page 51-52; 92pp; English.  
 FT  
 FT The invention relates to a nucleic acid vaccine comprising one or more  
 FT tumour antigen-encoding nucleic acids and one or more cytokine adjuvant-  
 FT encoding nucleic acids. The tumour antigen encoded by the vaccine is  
 FT mucin 1 (MUC-1), the kallikrein KLK2, or prostate specific antigen (PSA,  
 FT also known as KLK3), and the cytokine adjuvant encoded can be interleukin  
 FT -12 (IL-12), granulocyte macrophage-colony stimulating factor (GM-CSF),  
 FT or especially interleukin-18 (IL-18). The antigen-encoding nucleic acid  
 FT is preferably under the control of a promoter such as the cytomegalovirus  
 FT immediate early promoter, the dihydrofolate reductase promoter or the  
 FT early or late SV40 promoters. The invention also encompasses the method  
 FT of eliciting an immune response to a tumour antigen in a mammal using the  
 FT vaccine of the invention. Coexpression of the antigen and adjuvant  
 FT induces a humoral or cellular response to the tumour antigen, generating  
 FT an immune response useful for treatment or prophylaxis of cancers. The  
 FT present sequence represents an interleukin-18 (IL-18) polypeptide which  
 FT is specifically claimed for use in the vaccine of the invention.  
 FT  
 FT SQ Sequence 157 AA;  
 FT  
 FT Query Match 99.9%; Score 811; DB 6; Length 157;  
 FT Best Local Similarity 99.4%; Pred. No. 9.8e-83;  
 FT Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLSKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTTIFIISMYKDSQPRGM 60  
 DB 1 YFGKLSKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTTIFIISMYKDSQPRGM 60  
 QY 61 AVTISVKCEKISLSCENKIISFKENPPDNIKDTKSDIIFQSVPGHDKMKQFESSY 120  
 DB 61 AVTISVKCEKISLSCENKIISFKENPPDNIKDTKSDIIFQSVPGHDKMKQFESSY 120  
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
 DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 11  
 ADA50610  
 ID ADA50610 standard; protein; 157 AA.  
 XX  
 AC ADA50610;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Human mature consensus interleukin-18 (IL-18), SEQ ID NO:65.  
 XX  
 XX Nucleic acid vaccine; DNA vaccine; tumour antigen; cytokine adjuvant;

KW humoral response; cellular response; immune response; immunotherapy;  
 KW cancer; cytostatic; vaccine; gene therapy; interleukin-18; IL-18; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003031569-A2.  
 XX  
 PD 17-APR-2003.  
 XX  
 XX 18-SEP-2002; 2002WO-US029640.  
 PF  
 XX 10-OCT-2001; 2001US-0328371P.  
 PR  
 XX (CENZ ) CENTOCOR INC.  
 PA  
 XX Snyder L, Scallion B, Knight DM, McCarthy SG, Goletz TJ;  
 PI Branigan PJ;  
 PI WPI: 2003-393437/37.  
 XX N-PSDB; ADA50608.  
 DR  
 XX New nucleic acid vaccine, useful for eliciting an immune response to a  
 XX cancer associated tumor protein in a mammal.  
 FT  
 FT Claim 1b; Page 51-52; 92pp; English.  
 PS  
 XX The invention relates to a nucleic acid vaccine comprising one or more  
 XX tumour antigen-encoding nucleic acids and one or more cytokine adjuvant-  
 CC encoding nucleic acids. The tumour antigen encoded by the vaccine is  
 CC mucin 1 (MUC-1), the kallikrein KLK2, or prostate specific antigen (PSA,  
 CC also known as KLK3), and the cytokine adjuvant encoded can be interleukin  
 CC -12 (IL-12), granulocyte macrophage-colony stimulating factor (GM-CSF),  
 CC or especially interleukin-18 (IL-18). The antigen-encoding nucleic acid  
 CC is preferably under the control of a promoter such as the cytomegalovirus  
 CC immediate early promoter, the dihydrofolate reductase promoter or the  
 CC early or late SV40 promoters. The invention also encompasses the method  
 CC of eliciting an immune response to a tumour antigen in a mammal using the  
 CC vaccine of the invention. Coexpression of the antigen and adjuvant  
 CC induces a humoral or cellular response to the tumour antigen, generating  
 CC an immune response useful for treatment or prophylaxis of cancers. The  
 CC present sequence represents an interleukin-18 (IL-18) polypeptide which  
 CC is specifically claimed for use in the vaccine of the invention.  
 CC  
 XX SQ Sequence 157 AA;

Query Match 99.9%; Score 811; DB 6; Length 157;  
 Best Local Similarity 99.4%; Pred. No. 9.8e-83;  
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 YFGKLSKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTTIFIISMYKDSQPRGM 60  
 DB 1 YFGKLSKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTTIFIISMYKDSQPRGM 60  
 QY 61 AVTISVKCEKISLSCENKIISFKENPPDNIKDTKSDIIFQSVPGHDKMKQFESSY 120  
 DB 61 AVTISVKCEKISLSCENKIISFKENPPDNIKDTKSDIIFQSVPGHDKMKQFESSY 120  
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
 DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 12  
 ABR83372  
 ID ABR83372 standard; protein; 157 AA.  
 XX  
 AC ABR83372;  
 XX  
 DT 07-OCT-2003 (first entry)  
 XX  
 DE Human interleukin 18 amino acid sequence.  
 XX  
 XX Human; interleukin 1; IL-1; interleukin 18; IL-18; mutant; mutein;

KW mutant interleukin 18; MUT-IL-18; antiinflammatory; gene therapy;  
 KW inflammatory disorder.  
 XX Homo sapiens.  
 XX WO2003057821-A2.  
 XX 17-JUL-2003.  
 XX 25-OCT-2002; 2002WO-US034235.  
 XX 26-OCT-2001; 2001US-0335880P.  
 XX (CENZ ) CENTOCOR INC.  
 XX Heavner GA, Snyder LA, McCarthy SG;  
 XX WPI; 2003-577517/54.  
 XX New MUT-IL-18 nucleic acid, useful for preparing a composition for  
 PT diagnosing or treating a MUT-IL-18 related condition, e.g., inflammatory  
 PT disorder.  
 XX Example 3; Page 74; 97pp; English.  
 XX The present invention describes a mutant interleukin 18 (MUT-IL-18)  
 CC nucleic acid comprising or complementary to at least one polynucleotide  
 CC encoding an IL-18 amino acid sequence comprising at least one mutation  
 CC corresponding to at least one substitution selected from the group  
 CC consisting of Thr10 for Ser10, Val12 for Ile12, Ser45 for Thr45, Tyr47  
 CC for Phe47, Phe52 for Tyr52, Val64 for Ile64, Tyr101 for Phe101, Val5 for  
 CC Leu5, Val20 for Leu20, Ile20 for Leu20, Tyr21 for Phe21, Val22 for Ile22,  
 CC Ile66 for Val66, Thr72 for Ser72, or Phe148 for Ser148. Also described:  
 CC (1) a MUT-IL-18 polypeptide; (2) a MUT-IL-18 antibody; (3) a MUT-IL-18  
 CC vector comprising the MUT-IL-18 nucleic acid; (4) a MUT-IL-18 host cell  
 CC comprising the MUT-IL-18 nucleic acid; (5) a composition comprising a MUT  
 CC -IL-18 nucleic acid, polypeptide or antibody; (6) diagnosing or treating  
 CC a MUT-IL-18 related condition in a cell, tissue, organ or animal; (7) a  
 CC device comprising MUT-IL-18 nucleic acid, polypeptide or antibody and  
 CC that is suitable for contacting or administering the MUT-IL-18 nucleic  
 CC acid, polypeptide or antibody; (8) an article of manufacture for human  
 CC pharmaceutical or diagnostic use; and (9) producing the MUT-IL-18 nucleic  
 CC acid, polypeptide or antibody. MUT-IL-18 has antiinflammatory activity  
 CC and can be used in gene therapy. The MUT-IL-18 nucleic acid can be used  
 CC for preparing a composition for diagnosing or treating a MUT-IL-18  
 CC related condition, e.g. inflammatory disorder. The present sequence  
 CC represents a human IL-18 amino acid sequence given in an example from the  
 CC present invention  
 XX Sequence 157 AA;

Query Match 99.9%; Score 811; DB 6; Length 157;  
 Best Local Similarity 99.4%; Pred. No. 9.8e-83;  
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60  
 Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60  
 QY 61 AVTISVKCEKISXLSCKENKLIISFKEMPPDNIDKTSDIIFQFORSVPGHDKMKQFESSY 120  
 Db 61 AVTISVKCEKISXLSCKENKLIISFKEMPPDNIDKTSDIIFQFORSVPGHDKMKQFESSY 120  
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSINFVTQVNE 157  
 Db 121 EGYFLACEKERDLFKLILKKEDELGDRSINFVTQVNE 157

RESULT 13  
 ADE06775  
 ID ADE06775 standard; protein; 157 AA.  
 XX  
 AC ADE06775;

XX 29-JAN-2004 (first entry)  
 XX Human anti-diabetes Ig derived protein SEQ ID NO:3.  
 DE human; Ig; diabetes; complementarity-determining region; CDR;  
 XX antidiabetic; ophthalmological; neuroprotective; gene therapy;  
 KW diabetes mellitus; insulin resistance; hyperglycaemia; hypoglycaemia;  
 KW pancreatitis; Cushing's syndrome; acanthosis nigricans; retinopathy;  
 KW nephropathy; polyneuropathy; ulcer; infection.  
 XX Homo sapiens.  
 OS WO2003083071-A2.  
 XX 09-OCT-2003.  
 XX 26-MAR-2003; 2003WO-US009459.  
 XX 26-MAR-2002; 2002US-0367902P.  
 XX (CENZ ) CENTOCOR INC.  
 XX Griswold DE, Li J, Li L;  
 XX WPI; 2003-804047/75.  
 XX New isolated anti-diabetes immunoglobulin (Ig)-derived protein,  
 PT comprising at least one complementarity determining region (CDR) useful  
 PT for treating a diabetes-related condition, e.g. type I or II diabetes  
 PT mellitus, retinopathy.  
 XX Claim 1; SEQ ID NO 3; 84pp; English.  
 XX The invention relates to a novel isolated anti-diabetes immunoglobulin  
 CC (Ig)-derived protein, comprising at least one complementarity-determining  
 CC region (CDR). A protein of the invention has antidiabetic,  
 CC ophthalmological, and neuroprotective activity, and may have a use in  
 CC gene therapy. The protein, nucleic acid, composition and methods of the  
 CC invention are useful for treating a diabetes-related condition, e.g. type  
 CC I or II diabetes mellitus, insulin resistance, hyperglycaemia,  
 CC hypoglycaemia, pancreatitis, Cushing's syndrome, acanthosis nigricans,  
 CC retinopathy, nephropathy, polyneuropathy, ulcers, or infections. The  
 CC present sequence represents an anti-diabetes Ig derived protein of the  
 CC invention.  
 XX Sequence 157 AA;

Query Match 99.9%; Score 811; DB 7; Length 157;  
 Best Local Similarity 99.4%; Pred. No. 9.8e-83;  
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60  
 Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60  
 QY 61 AVTISVKCEKISXLSCKENKLIISFKEMPPDNIDKTSDIIFQFORSVPGHDKMKQFESSY 120  
 Db 61 AVTISVKCEKISXLSCKENKLIISFKEMPPDNIDKTSDIIFQFORSVPGHDKMKQFESSY 120  
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSINFVTQVNE 157  
 Db 121 EGYFLACEKERDLFKLILKKEDELGDRSINFVTQVNE 157

RESULT 14  
 AAY85167  
 ID AAY85167 standard; protein; 158 AA.  
 XX  
 AC AAY85167;  
 XX  
 DT 23-JUN-2000 (first entry)  
 XX



```

DE Human interleukin-18 (IL-18) amino acid sequence.
XX
KW Interleukin-18; production; IL-18; human; medical injection product.
XX
OS Homo sapiens.
XX
PN CN1243130-A.
XX
PD 02-FEB-2000.
XX
PF 24-JUL-1998; 98CN-00103307.
XX
PR 24-JUL-1998; 98CN-00103307.
XX
PA (WUGG/) WU G.
XX
PI Wu G, Liu Z;
XX
DR WPI; 2000-340020/30.
XX
N-PSDB; AAA10526.
XX
PT Preparation method for engineering bacteria for recombination of human
leucocyte medium-18 and its product thereof.
XX
PS Claim 1; Page 2; 17pp; English.
XX
CC This sequence represents the human interleukin-18 (IL-18) amino acid
sequence. The invention relates to a method for engineering bacterium for
recombination of human IL-18 and a method for the preparation of IL-18. A
primer containing a restriction endonuclease site can be used to
accurately obtain the IL-18 gene containing 474 nucleotides, and uses the
stop codon preferred by coli bacillus to raise the expression rate. The
method uses a high-amplification culture medium to increase the
expression level and only requires a one-step purification process to
obtain a medical injection-pure product
XX
SQ Sequence 158 AA;
Query Match 99.9%; Score 811; DB 3; Length 158;
Best Local Similarity 99.4%; Pred. No. 9.9e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNAPRTFIISMYKDSQPRGM 60
DB 2 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNAPRTFIISMYKDSQPRGM 61
QY 61 AVTISVKCEKISXLSCEKNIISFKENPPDNINKDTKSDIIFQFQSVPGHDKMKQFESSY 120
DB 62 AVTISVKCEKISTLSCENKIISFKENPPDNINKDTKSDIIFQFQSVPGHDKMKQFESSY 121
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 122 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 158
RESULT 15
ADA50614
ID ADA50614 standard; protein; 177 AA.
XX
AC ADA50614;
XX
DT 20-NOV-2003 (first entry)
XX
DE Mature consensus IL-18/LC signal sequence fusion protein, SEQ ID NO:69.
XX
KW Nucleic acid vaccine; DNA vaccine; tumour antigen; cytokine adjuvant;
KW humoral response; cellular response; immune response; immunotherapy;
KW cancer; cytostatic; vaccine; gene therapy; interleukin-18; IL-18; human.
XX
OS Chimeric.
OS Homo sapiens.
XX
FH Key Location/Qualifiers

```

```

FT Peptide 1..20
FT /label= Human_ILC_signal_sequence
FT Protein 21..177
FT /label= Mature_consensus_IL-18
XX
FN WO2003031569-A2.
XX
PD 17-APR-2003.
XX
PF 18-SEP-2002; 2002WO-US029640.
XX
PR 10-OCT-2001; 2001US-0328371P.
XX
PA (CENZ ) CENTOCOR INC.
XX
PI Snyder L, Scallon B, Knight DM, Mccarthy SG, Goletz TJ;
PI Branigan PJ;
XX
DR WPI; 2003-393437/37.
DR N-PSDB; ADA50611.
XX
PT New nucleic acid vaccine, useful for eliciting an immune response to a
cancer associated tumor protein in a mammal.
XX
PS Claim 1b; Page 53; 92pp; English.
XX
CC The invention relates to a nucleic acid vaccine comprising one or more
tumour antigen-encoding nucleic acids and one or more cytokine adjuvant-
encoding nucleic acids. The tumour antigen encoded by the vaccine is
mucin 1 (MUC-1), the kallikrein KLK2, or prostate specific antigen (PSA,
also known as KLK3), and the cytokine adjuvant encoded can be interleukin
-12 (IL-12), granulocyte macrophage-colony stimulating factor (GM-CSF),
or especially interleukin-18 (IL-18). The antigen-encoding nucleic acid
is preferably under the control of a promoter such as the cytomegalovirus
immediate early promoter, the dihydrofolate reductase promoter or the
early or late SV40 promoters. The invention also encompasses the method
of eliciting an immune response to a tumour antigen in a mammal using the
vaccine of the invention. Coexpression of the antigen and adjuvant
induces a humoral or cellular response to the tumour antigen, generating
an immune response useful for treatment or prophylaxis of cancers. The
present sequence represents an interleukin-18 (IL-18) polypeptide which
is specifically claimed for use in the vaccine of the invention.
XX
SQ Sequence 177 AA;
Query Match 99.9%; Score 811; DB 6; Length 177;
Best Local Similarity 99.4%; Pred. No. 1.2e-82;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNAPRTFIISMYKDSQPRGM 60
DB 21 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNAPRTFIISMYKDSQPRGM 80
QY 61 AVTISVKCEKISXLSCEKNIISFKENPPDNINKDTKSDIIFQFQSVPGHDKMKQFESSY 120
DB 81 AVTISVKCEKISTLSCENKIISFKENPPDNINKDTKSDIIFQFQSVPGHDKMKQFESSY 140
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 141 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 177
Search completed: August 19, 2004, 13:35:04
Job time : 54 secs

```



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2004, 13:33:10 ; Search time 16 Seconds  
(without alignments)  
943.879 Million cell updates/sec

Title: US-09-716-356A-6  
Perfect score: 812  
Sequence: 1 YFGKLESKLVIRNLNDQVL.....LKKEDELGDRSIMFTVQNE 157

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues  
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*  
1: Pir1:\*  
2: Pir2:\*  
3: Pir3:\*  
4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	515	63.4	132	2 S60226	cytokine IGIF - mouse
2	85	10.5	381	2 T40341	hypothetical prote
3	82	10.1	263	2 T39487	hypothetical prote
4	81.5	10.0	270	1 S10532	interleukin-1 alph
5	80.5	9.9	866	2 C71509	probable DNA polym
6	79	9.7	452	2 D64583	hypothetical prote
7	78.5	9.7	204	2 T44357	hypothetical prote
8	78	9.6	473	2 T32038	hypothetical prote
9	77.5	9.5	1251	2 A56677	neutrophil cell cycl
10	77	9.5	364	2 A81261	probable periplasm
11	76	9.4	632	2 T00679	hypothetical prote
12	76	9.4	747	2 E84698	hypothetical prote
13	75.5	9.3	132	2 S15661	(2'-5')oligo(A) sy
14	75.5	9.3	270	2 T32038	interleukin-1 alph
15	75.5	9.3	1036	2 H64245	hypothetical prote
16	75.5	9.3	1663	1 C3MS	complement C3 prec
17	75	9.2	1064	1 S57450	protein-tyrosine k
18	75	9.2	2470	2 I50726	cation-independent
19	74.5	9.2	334	2 T04198	hypothetical prote
20	74.5	9.2	389	2 B69277	TRK potassium upre
21	74.5	9.2	467	2 A48713	serine/threonine-s
22	74.5	9.2	1228	2 A57384	multimerin, endoth
23	74.5	9.2	1510	2 T16927	hypothetical prote
24	74	9.1	245	2 B90488	hypothetical prote
25	74	9.1	361	2 E96904	mIND family ATPase
26	74	9.1	376	2 T24925	hypothetical prote
27	74	9.1	467	2 I49609	proto-oncogene pro
28	74	9.1	467	2 A47388	serine/threonine p
29	74	9.1	680	2 A28121	major merozoite su

30	74	9.1	810	2 B71639	virb4 protein prec
31	74	9.1	1772	2 A45532	major merozoite su
32	73.5	9.1	268	2 H85641	probable small sub
33	73.5	9.1	268	2 C90781	probable small sub
34	73	9.0	418	2 D82932	seryl-tRNA synthet
35	73	9.0	447	2 T26293	hypothetical prote
36	72.5	8.9	268	1 B24073	interleukin-1 alph
37	72.5	8.9	313	2 C96528	protein F27J15.10
38	72.5	8.9	436	2 G97701	polynucleotide ade
39	72.5	8.9	475	2 T32036	hypothetical prote
40	72.5	8.9	888	2 A38539	pl01 protein precu
41	72.5	8.9	1246	2 S60954	probable membrane
42	72.5	8.9	1294	2 T48349	KIN2 protein - Ara
43	72.5	8.9	1997	2 F71607	DNA helicase II BR
44	72	8.9	284	2 B90051	hypothetical prote
45	72	8.9	1613	2 S39059	protein BRG1 - hum

ALIGNMENTS

RESULT 1  
S60226  
cytokine IGIF - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 10-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 20-Jun-2000  
C;Accession: S60226  
R;Okamura, H.; Tsutsui, H.; Komatsu, T.; Yutsudo, M.; Hakura, A.; Tanimoto, T.; Torigoe, Nature 378, 88-91, 1995  
A;Title: Cloning of a new cytokine that induces IFN-gamma production by T cells.  
A;Reference number: S60226; MUID:96061009; PMID:7477296  
A;Accession: S60226  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-192 <OKA>  
A;Cross-references: EMBL:D49949; NID:g1064822; PIDN:BAA08705.1; PID:g1064823  
C;Superfamily: Mus musculus cytokine IGIF

Query Match	63.4%	Score	515;	DB	2;	Length	192;
Best Local Similarity	64.9%	Pred. No.	2.8e-42;				
Matches	100;	Conservative	27;	Mismatches	25;	Indels	2;
						Gaps	2;
QY	2	FGKLESKLVIRNLNDQVLFDQGNPLPDMEDMTDSDCRNAPRTIIFIISMYKDSQRGMA	61				
Db	37	FGRLHCTTAVIRINDQVLFDVK-RQVPFDMTDIDQSASEPQTRLIIYMKDSEVRGLA	95				
QY	62	VTISVCKEIKSLSCENKIISPKEMNPPDNIDKTDIIFFORSVPDHNMQOFESSSVE	121				
Db	96	VTLSVCKSKMTSLSCXNKIISFEEMDPDENIDDIQSDLIFFQKRVPGH-NKMEFESSLYE	154				
QY	122	GYFLACEKERDLFKLILKKKDELGDRSIMFTVQN	155				
Db	155	GHEFLACQKEDDAFKLILKKKDKGVNFTLTN	188				

RESULT 2  
T40341  
hypothetical protein SPBC3B9.02c - fission yeast (Schizosaccharomyces pombe)  
C;Species: Schizosaccharomyces pombe  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
C;Accession: T40341  
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M. submitted to the EMBL Data Library, March 1997  
A;Reference number: Z21922  
A;Accession: T40341  
A;Status: preliminary; translated from GB/EMBL/DBU  
A;Molecule type: DNA  
A;Residues: 1-381 <WOO>  
A;Cross-references: EMBL:AL022070; PIDN:CAAL7782.1; GSPDB:GN00067; SPDB:SPBC3B9.02c  
A;Experimental source: strain 972h-; cosmid c3B9  
C;Genetics:  
A;Gene: SPDB:SPBC3B9.02c





C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000  
A:Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hyp A:Reference number: AB1250; MUID:20150912; PMID:10688204  
A:Accession: AB1261  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-364 <PAR>  
A:Cross-references: GB:AL111168; NID:G6968971; PIDN:CAB73631.1; PID:G696906  
A:Experimental source: serotype O2, strain NCTC 11168  
C:Genetics:  
A:Gene: Cj1643

Query Match 9.5%; Score 77; DB 2; Length 364;  
Best Local Similarity 24.8%; Pred. No. 8.9; Mismatches 40; Indels 54; Gaps 9;  
Matches 38; Conservative 21

QY 12 IRNLNDQVLFIDQGNRPLFEDMTDSDCRD-NAPRTIFIISMYK----DSQPR----- 58  
Db 211 LRKLEKILFADRGSTLYFQVLRDN--MDLNISTEVFAKDLKFNLPDCKPKKTNFTS 268  
QY 59 --GMAVTISVKCEKI-----SXLSCEKII-SFKEMNPPDN----- 92  
Db 269 NLGLTVNASLVVTKIDPKSKVSNAGFMVGDKILRVNIIINNFXEL---QNTLSAGNDFS 325  
QY 93 ----KDTKSDIIFFQSRVPEGH-----DNKMQF 115  
Db 326 ILIERKSTKLPLSNFNNELGWNANGGDKGFQF 358

RESULT 11  
T00679  
hypothetical protein At2g43990 [imported] - Arabidopsis thaliana  
N:Alternate names: hypothetical protein F6E13.12  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C:Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 23-Mar-2001  
C:Accession: T00679; A84873  
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, June 1998  
A:Description: Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence.  
A:Reference number: A84873  
A:Accession: T00679  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-632 <ROU>  
A:Cross-references: EMBL:AC004005; NID:G3212846; PID:G3212856  
A:Experimental source: cultivar Columbia  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: A84873  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-632 <STO>  
A:Cross-references: GB:AE002093; NID:G3212856; PIDN:AAC23407.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: At2g43990; F6E13.12  
A:Map position: 2

Query Match 9.4%; Score 76; DB 2; Length 632;  
Best Local Similarity 25.6%; Pred. No. 21; Mismatches 40; Indels 30; Gaps 9;  
Matches 34; Conservative 29

QY 28 PLFEDMTDSD-CRDNAPRTIFIISMYKDSQPRGMATISVKCEK-----ISXLSCEK 79  
Db 368 PLSDRSASSDLGNISGRSLSPMDIYKETTTR---ISSLSLSPNLPFRFRFHLSSCDGE 424  
QY 80 IISFK-----ENPPNIDKTSDIIFQSRYP--CHDNKMQF--ESSSVEGYF-LACEK 129  
Db 425 AGAFDTSPTELDPSHLAGDKSSPL-----SVDTLGSENVIOTPRNSNSGDFNIFGLSCSQ 480

QY 130 ERDLFKLILKXED 142  
Db 481 AE-----IQKXD 488

RESULT 12  
E84698  
hypothetical protein At2g29620 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C:Accession: E84698  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: E84698  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-747 <STO>  
A:Cross-references: GB:AE002093; NID:G3582336; PIDN:AAC35233.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: At2g29620  
A:Map position: 2

Query Match 9.4%; Score 76; DB 2; Length 747;  
Best Local Similarity 24.7%; Pred. No. 26; Mismatches 59; Indels 22; Gaps 7;  
Matches 36; Conservative 29

QY 4 KLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRD-NAPRTIFIISMYKDSQPRGMAT 63  
Db 102 KKHQOQSVRRNARKV-----BEVGKWDSSQASDEBERGKVILTLTYGEVLPE---T 150  
QY 64 ISVCKEIKSXLSCEKNIISFKEMNPPDNIDKTSDIIFQSR--SVPGHDKMQFE---SS 118  
Db 151 ITPDMEKFK---RERTLLVAENFVDSVLNDRHDLVELERLISVDG-DDESEVCSSS 205  
QY 119 SYEGYFLACERDLFKLILK-KEDE 143  
Db 206 SSEGEKEEERREDVSKVVAVMTDD 231

RESULT 13  
S15661  
(2'-5')oligo(A) synthetase (EC 2.7.7.-) L1 - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Dec-1993 #sequence\_revision 02-Jun-1994 #text\_change 16-Jul-1999  
C:Accession: S15661; S19108  
R:Rutherford, M.N.; Kumar, A.; Nissim, A.; Chebath, J.; Williams, B.R.G. Nucleic Acids Res. 19, 1917-1924, 1991  
A:Title: The murine 2-5A synthetase locus: three distinct transcripts from two linked ge A:Reference number: S15660; MUID:91232962; PMID:1709495  
A:Accession: S15661  
A:Molecule type: mRNA  
A:Residues: 1-192 <RUT>  
A:Cross-references: EMBL:X55982  
R:Williams, B. submitted to the EMBL Data Library, September 1990  
A:Reference number: S19108  
A:Accession: S19108  
A:Molecule type: mRNA  
A:Residues: 1-175, 'L', 177-192 <WIL>  
A:Cross-references: EMBL:X55982; NID:G49714; PIDN:CAA39455.1; PID:G49715  
C:Superfamily: oligo(A) synthetase  
C:Keywords: nucleotidyltransferase

Query Match 9.3%; Score 75.5; DB 2; Length 192;  
Best Local Similarity 23.2%; Pred. No. 5.8; Mismatches 50; Indels 65; Gaps 9;  
Matches 42; Conservative 24

QY 3 GKLESKLSVIRN-----LNDQVLFIDQGNRPLFEDMTDSDCRD-NAPRTIFIISMYK 54

```

Db      11  GRSDADLVFNILNLTSPEDQINQGVLLKEIKQLCEVQHERRC----- 54
QY      55  SQPRGMVAVTSVKCEKISXISCENKIIISPKEMNPPDNIKDTKSDII----- 100
Db      55  -----GVKPEVHSLSPNSRALSFK-LSAPDILLKEVKFDVLPAYDILLDHLNLKK 103
QY      101  -----FFQR---SVP-GHDNKKMQPFESSYEGYFLACE--KERDLFKLI-----LKKDEELG 145
Db      104  PNOQFYANLISGVPAKGEGKLSICFMGLQKLYFLNCRPTKUKRLRLVTHWYQLCKE-KLG 162
QY      146  D 146
Db      163  D 163

RESULT 14
I46620
interleukin-1 alpha precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 04-Feb-2000
C;Accession: I46620
R;Maliszewski, C.
Nucleic Acids Res. 14, 4282, 1990
A;Title: Nucleotide sequence of porcine interleukin-1 alpha.
A;Reference number: I46620
A;Accession: I46620
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-270 <NAL>
A;Cross-references: GB:M86730; NID:g164622; PIDN:AAA73198.1; PID:g164623
C;Superfamily: interleukin-1
C;Keywords: lipoprotein; myristylation
F;1-112/Domain: propeptide #status predicted <PRO>
F;113-270/Product: interleukin-1 alpha #status predicted <ILI>
F;82,83/Binding site: myristate (lys) (covalent) #status predicted

Query Match          9.3%; Score 75.5; DB 2; Length 270;
Best Local Similarity 22.0%; Pred. No. 8.7;
Matches 29; Conservative 32; Mismatches 58; Indels 13; Gaps 6;

QY      8  KLSVIRNLNDQVLFDQGNRPLFEDMTD----SDCRDNAPRTI-FIISMYKDSQPRGMV 62
Db      123  KYNFMRVINHQIINDARNQSIIRDPSQYILMAVINLDEAVKFDMAAYTSNDDSQLPV 182
QY      63  TISVKCEKISXISCEN--KIISPKEM-NPDDNIDKTSDIIFQORSVPGHDKMKQPFESS 119
Db      183  TLRIS-ETRLFVSAQNEDEPVLKELPTEKTIKDTSLFFWEK----HGNMDYFKSAA 237
QY      120  YEGYFLACEKER 131
Db      238  HPKLLIATRQEK 249

RESULT 15
H64245
hypothetical protein MG414 - Mycoplasma genitalium
C;Species: Mycoplasma genitalium
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 02-Mar-2001
C;Accession: H64245; G64245
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346; PMID:7569993
A;Accession: H64245
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1036 <TIGR>
A;Cross-references: GB:U39727; GB:I43967; NID:g1046127; PID:g1046129; TIGR:MG414
A;Experimental source: strain G-37
A;Accession: G64245
```

```

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 'M',310-1036 <TIG2>
A;Cross-references: GB:U39727; GB:I43967; NID:g1046127; PID:g1046128; TIGR:MG413
A;Experimental source: strain G-37
C;Genetics:
A;Genetic code: SGC3
A;Start codon: GTG
C;Superfamily: hypothetical protein MG413

Query Match          9.3%; Score 75.5; DB 2; Length 1036;
Best Local Similarity 21.9%; Pred. No. 43;
Matches 33; Conservative 32; Mismatches 65; Indels 21; Gaps 6;

QY      14  NLNDQVLFDQGNRPLFED--MTDSDCRDNAPRTI-FIISMYKDSQPRGMVAVTSVKCEK- 70
Db      845  SLNDEQLLVKLNITLSEKRLQTTKNVRFNLKKNKFINIHLENKQNFNLVFDVDRSKKL 904
QY      71  -ISXISCENKIIISPKEMNPPDNIDKTSDIIFQORSVPGHDKMKQPFESSYEGYFLACE 129
Db      905  FIKGVNNDNQVFLISY-----DLKITNNQTLIV-DANGFDNSIWFDTIS-----EN 950
QY      130  ERDLFKLI---LKKDELGDRSIMFTVQNE 157
Db      951  QTQLFKALSPYLKQNNLQFKRVDPDFNLKSQD 981

Search completed: August 19, 2004, 13:36:45
Job time : 17 secs
```





GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2004, 13:31:14 ; Search time 13 Seconds  
(without alignments)  
628.847 Million cell updates/sec

Title: US-09-716-356A-6

Perfect score: 812  
Sequence: 1 YFGKLESKLVIRNLDQVL.....LKKDELGDRSIMFTVQNEED 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	811	99.9	193	IL18_HUMAN	Q14116 homo sapien
2	659	81.2	193	IL18_HORSE	Q9xsq7 equus caball
3	654	80.5	193	IL18_BOVIN	Q9tu73 bos taurus
4	637	78.4	192	IL18_PIG	Q19073 sus scrofa
5	633	75.5	193	IL18_CANFA	Q9xsr0 canis famil
6	545	63.4	192	IL18_MOUSE	P70380 mus musculu
7	514.5	63.4	194	IL18_RAT	P97636 rattus norv
8	178.5	22.0	196	IL18_CHICK	Q8qf98 gallus gall
9	88	10.8	4705	PAT2_DROME	Q9vw71 drosophila
10	81.5	10.0	270	IL1A_PIG	P18430 sus scrofa
11	81	10.0	267	IL1A_RABIT	P04822 oryctolagus
12	80	9.9	1449	DPO3_CLOPE	Q8xjr3 clostridium
13	79.5	9.8	664	DNAK_CHLCV	Q824b2 chlamydomphi
14	77.5	9.5	674	MUTL_CLOPE	Q8x186 clostridium
15	76.5	9.4	270	IL1A_HORSE	Q28385 equus caball
16	75.5	9.3	192	OASB_MOUSE	Q60856 mus musculu
17	75.5	9.3	1036	Y414_MYCGE	P047653 mycoplasma
18	75.5	9.3	1663	CO3_MOUSE	P01027 mus musculu
19	74.5	9.2	1228	EMI4_HUMAN	Q13201 homo sapien
20	74	9.1	467	M3K8_MOUSE	Q07174 mus musculu
21	74	9.1	467	M3K8_RAT	Q63562 rattus norv
22	74	9.1	1772	MSPI_PLAYO	P13828 plasmodium
23	73	9.0	270	IL1A_FELCA	Q46613 felis silve
24	73	9.0	418	SYS_UREPA	Q9pr38 ureaplasma
25	73	9.0	426	YCXK_ASTLO	P58151 astasia lon
26	72.5	8.9	313	COLA_ARATH	Q9m9b3 arabidopsis
27	72.5	8.9	412	UVSE_CLOPE	Q8xip3 clostridium
28	71.5	8.8	268	IL1A_BOVIN	P08831 bos taurus
29	71.5	8.8	467	M3K8_HUMAN	P41279 homo sapien
30	71.5	8.8	527	RAG2_HUMAN	P55895 homo sapien
31	71	8.7	700	NONA_DROME	Q04047 drosophila
32	70.5	8.7	245	KDSB_FUSNN	Q8rfa8 fusobacteri
33	70.5	8.7	268	IL1A_CAPHI	P79161 capra hircu

#### RESULT 1

IL18_HUMAN					
ID	IL18_HUMAN	STANDARD;	PRT;	193 AA.	
AC	Q14116;	O75599;			
DT	15-JUL-1998	(Rel. 36, Created)			
DT	15-JUL-1998	(Rel. 36, Last sequence update)			
DT	10-OCT-2003	(Rel. 42, Last annotation update)			
DE	Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)				
DE	[IFN-gamma-inducing factor] (Interleukin-1 gamma) (IL-1 gamma).				
OS	IL18 OR IGIF.				
GN	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
[1]	TaxID=9606;				
RN	SEQUENCE FROM N.A.				
RP	TISSUE=Liver;				
RC	MEDLINE=96247646; PubMed=8666798;				
RX	Ushio S., Namba M., Okura T., Hattori K., Nukada Y., Akita K.,				
RA	Tanabe F., Konishi K., Micallef M., Fujii M., Torigoe K., Tanimoto T.,				
RA	Fukuda S., Ikeda M., Okamura H., Kurimoto M.;				
RT	"Cloning of the cDNA for human IFN-gamma-inducing factor, expression				
RT	in Escherichia coli, and studies on the biologic activities of the				
RT	protein.";				
RL	J. Immunol. 156:4274-4279(1996).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RT	Yong D., Guixin D., Lihua H., Haitao W.;				
RT	"Cloning and sequencing of the cDNA for precursor hIL-18.";				
RT	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RL	Liu J., Peng X., Yuan J., Qiang B.;				
RT	"Cloning of human interleukin 18 cDNA.";				
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Urinary bladder;				
RX	MEDLINE=22388257; PubMed=12477932;				
RA	Strausberg R.L., Feilgold E.A., Grouse L.H., Derge J.G., Schuler G.D.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,				
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahney J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,				
RA	Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smailus D.E.,				
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;				

34	70.5	8.7	644	1	YGM4_YEAST	P53129 saccharomyc
35	70.5	8.7	659	1	DNK_CHLAB	Q8gh79 chlamydophi
36	70	8.6	198	1	VS11_ROTAR	P17467 rabbit roca
37	70	8.6	1647	1	SN24_HUMAN	P51532 homo sapien
38	70	8.6	2663	1	CENE_HUMAN	Q02224 homo sapien
39	70	8.6	4590	1	FATH_HUMAN	Q14517 homo sapien
40	69.5	8.6	268	1	IL1A_SHEEP	Q28579 ovis aries
41	69.5	8.6	351	1	RFL_TREPA	O83090 treponema p
42	69.5	8.6	375	1	YYC5_CAEEL	Q18610 caenorhabdi
43	69.5	8.6	582	1	CRTI_CAPAN	P80093 capsicum an
44	69.5	8.6	646	1	NOSZ_RALSO	Q8xqb8 ralstonia s
45	69.5	8.6	919	1	RPO2_CAPVK	P16716 capripoxvir

#### ALIGNMENTS

RT "Generation and initial analysis of more than 15,000 full-length  
 RL human and mouse cDNA sequences.";  
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP SEQUENCE OF 2-193 FROM N.A.  
 RC TISSUE=Peripheral blood;  
 RA Conti B., Kim S.J., Tinti C., Chun H.S., Joh T.H.;  
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS  
 CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I  
 CC CELLS.

CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the IL-1 family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; D49550; BA08706.1; -.  
 CC EMBL; AF077611; AAC27787.1; -.  
 CC EMBL; AY044641; AAK35950.1; -.  
 CC EMBL; BC007007; AAH07007.1; -.  
 CC EMBL; BC007461; AAH07461.1; -.  
 CC EMBL; U90434; AAB50010.1; -.  
 CC Genew; HGNC:5986; IL18.  
 CC MIM; 600953; -.  
 CC GO; GO:0005576; C:extracellular; TAS.  
 CC GO; GO:0016506; F:apoptosis activator activity; ISS.  
 CC GO; GO:0005125; F:cytokine activity; TAS.  
 CC GO; GO:0004871; F:signal transducer activity; TAS.  
 CC GO; GO:0001525; P:angiogenesis; IDA.  
 CC GO; GO:0007267; P:cell-cell signaling; TAS.  
 CC GO; GO:0042033; P:chemokine biosynthesis; TAS.  
 CC GO; GO:0042253; P:granulocyte macrophage colony-stimulating f. . .; TAS.  
 CC GO; GO:0006955; P:immune response; TAS.  
 CC GO; GO:0008625; P:induction of apoptosis via death domain rec. . .; ISS.  
 CC GO; GO:0042095; P:interferon-gamma biosynthesis; TAS.  
 CC GO; GO:0042231; P:interleukin-2 biosynthesis; TAS.  
 CC GO; GO:0042094; P:interleukin-2 biosynthesis; TAS.  
 CC GO; GO:0042104; P:positive regulation of activated T-cell pro. . .; IDA.  
 CC GO; GO:0030155; P:regulation of cell adhesion; IDA.  
 CC GO; GO:0030431; P:sleep; ISS.  
 CC GO; GO:0042092; P:T-helper 2 type immune response; TAS.  
 CC InterPro; IPR008996; Cytok IL1-like.  
 CC InterPro; IPR000975; Interleukin\_1.  
 CC SMART; SM00125; IL1; 1.  
 CC Cytokine.

FT PROPEP 1 36 BY SIMILARITY.  
 FT CHAIN 37 193 INTERLEUKIN-18.  
 FT CONFLICT 66 66 F -> L (IN REF. 2).  
 FT CONFLICT 86 86 S -> R (IN REF. 2).  
 FT CONFLICT 191 191 N -> S (IN REF. 2).  
 SQ SEQUENCE 193 AA; 22326 MW; 323C62C203788D55 CRC64;

Query Match 99.9%; Score 811; DB 1; Length 193;  
 Best Local Similarity 99.4%; Pred. No. 1.3e-68;  
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 60  
 Db YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 96  
 Qy 61 AVTISVKCEKISLSCENKIISFKEMNPPDNKTKSDIIFQSRVSGHDNKMQFESSY 120  
 Db AVTISVKCEKISTLSCKNKIISFKEMNPPDNKTKSDIIFQSRVSGHDNKMQFESSY 156

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
 Db 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193

## RESULT 2

IL18 HORSE  
 ID IL18 HORSE STANDARD; PRT; 193 AA.  
 AC Q9XSQ7;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)  
 DE (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).  
 OS IL18 OR IGIF.  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Nicolson L., Penha-Goncalves M.N., Keanie J.L., Logan N.A.,  
 RA Argyle D.J., Onions D.E.;  
 RL "Nucleotide sequence of equine interleukin 12 and 18 cDNAs.";  
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS  
 CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I  
 CC CELLS (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the IL-1 family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; Y11131; CA472013.1; -.  
 CC InterPro; IPR008996; Cytok\_IL1\_like.  
 KW Cytokine.  
 FT PROPEP 1 36 BY SIMILARITY.  
 FT CHAIN 37 193 INTERLEUKIN-18.  
 SQ SEQUENCE 193 AA; 22058 MW; 4D8153E9004EC4F CRC64;

Query Match 81.2%; Score 659; DB 1; Length 193;  
 Best Local Similarity 77.7%; Pred. No. 1.8e-54;  
 Matches 122; Conservative 21; Mismatches 14; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 60  
 Db YFGKLEPKLSIIRNLNDQVLFIDQGNQPVFEDMPSDCTDNAPQTVFIYMYKDSLTRL 96

Qy 61 AVTISVKCEKISLSCENKIISFKEMNPPDNKTKSDIIFQSRVSGHDNKMQFESSY 120  
 Db 97 AVTISVKCEKISTLSCKNKIISFKEMNPPDNKTKSDIIFQSRVSGHDNKMQFESSY 156

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
 Db 157 KGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193

## RESULT 3

IL18 BOVIN  
 ID IL18 BOVIN STANDARD; PRT; 193 AA.  
 AC Q9TU73;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)  
 DE (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

```
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20012648; PubMed=10547157;
RA Shoda L.K., Zarlega D.S., Hirano A., Brown W.C.;
RT "Cloning of a cDNA encoding bovine interleukin-18 and analysis of IL-
RT 18 expression in macrophages and its IFN-gamma-inducing activity.";
RL J. Interferon Cytokine Res. 19:1169-1177(1999).
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-1 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF124789; AAF08686.1; -.
DR InterPro: IPR008996; Cytok IL1 like.
DR InterPro: IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
FT PROPEP 1 36 BY SIMILARITY.
KW Cytokine.
FT CHAIN 37 193 INTERLEUKIN-18.
SQ SEQUENCE 193 AA; 22347 MW; 65720F199DEA49C4 CRC64;

Query Match 80.5%; Score 654; DB 1; Length 193;
Best Local Similarity 77.1%; Pred. No. 5.4e-54;
Matches 121; Conservative 23; Mismatches 13; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDVLFIDQGNRPFLFEDMTSDCRDNPRTIFIIISMYKDSQPRGM 60
DB 37 HFGLKPEKLSIIRNLNDVLFINQGVQVFEFDPDSDCDNAPQTIIYMYKDSLTRL 96
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 AVTISVCKEKISXLSCKENKIISFKENPPDNIDKTSDIIFQSVPGHDKMKQFESSY 120
DB 97 AVTISVQCKKMTSLSCNKNTLSFKENPPDNIDNEESDIIFQSVPGHDDKIQFESSLY 156
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 EGYFLACEKERDLFKLILKKEDELGDRSMFTVQNE 157
DB 157 KGFLACKENDLFKLILKQDDNRDKSVNFTVQNN 193
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
IL18_PIG
ID IL18_PIG STANDARD; PRT; 192 AA.
AC O19073;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Foss D.L., Murtaugh M.P.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Penha-Goncalves M.N., Logan N.A., Nicolson L., Onions D.E.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
```

```
RA Muneta Y., Mori Y.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE=Intestine;
RX MEDLINE=20260994; PubMed=10803849;
RA Fournout S., Dozois C.M., Yerle M., Pinton P., Fairbrother J.M.,
RA Oswald E., Oswald I.P.;
RT "Cloning, chromosomal location, and tissue expression of the gene for
RT pig interleukin-18.";
RL Immunogenetics 51:359-365(2000).
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-1 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U68701; AAC18415.1; -.
DR EMBL: Y11132; CAA72014.1; -.
DR EMBL; AB010003; BAA24135.1; -.
DR EMBL; AF191088; AAF71200.1; -.
DR GO; GO:0005576; C:extracellular; ISS.
DR GO; GO:0005125; P:cytokine activity; IMP.
DR GO; GO:0001525; P:angiogenesis; ISS.
DR GO; GO:0042033; P:chemokine biosynthesis; ISS.
DR GO; GO:0008625; P:induction of apoptosis via death domain rec. .; IDA.
DR GO; GO:0042095; P:interferon-gamma biosynthesis; IDA.
DR GO; GO:0042104; P:positive regulation of activated T-cell pro. .; ISS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR InterPro: IPR008996; Cytok IL1 like.
DR InterPro: IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
KW Cytokine.
FT PROPEP 1 35 BY SIMILARITY.
FT CHAIN 36 192 INTERLEUKIN-18.
SQ SEQUENCE 192 AA; 22026 MW; 881EA654E221A17A CRC64;

Query Match 78.4%; Score 637; DB 1; Length 192;
Best Local Similarity 75.2%; Pred. No. 2e-52;
Matches 118; Conservative 24; Mismatches 15; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDVLFIDQGNRPFLFEDMTSDCRDNPRTIFIIISMYKDSQPRGM 60
DB 36 YFGKLEPKLSIIRNLNDVLFINQGVQVFEFDPDSDCDNAPQTIIYMYKDSLTRL 95
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 AVTISVCKEKISXLSCKENKIISFKENPPDNIDKTSDIIFQSVPGHDKMKQFESSY 120
DB 96 AVTISVQCKKMTSLSCNKNTLSFKENPPDNIDEGNDIIFQSVPGHDDKIQFESSLY 155
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 EGYFLACEKERDLFKLILKKEDELGDRSMFTVQNE 157
DB 156 KGFLACKENDLFKLILKKEDEKCGDKSIFMTVQNN 192
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
IL18_CANFA
ID IL18_CANFA STANDARD; PRT; 193 AA.
AC O9XSRO;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Canis familiaris (Dog).
```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=99309818; PubMed=10380699;
RA Argyle D.J., McGillivray C., Nicolson L., Onions D.E.;
RT "Cloning, sequencing, and characterization of dog interleukin-18.";
RL Immunogenetics 49:541-543(1999).
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-1 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Y11133; CAA72015.1; -.
CC GO; GO:0005576; C:extracellular; TAS.
CC GO; GO:0016506; F:apoptosis activator activity; ISP.
CC GO; GO:0005125; P:cytokine activity; TAS.
CC GO; GO:0042033; P:chemokine biosynthesis; ISS.
CC GO; GO:0008625; P:induction of apoptosis via death domain rec. .; ISP.
CC GO; GO:0042035; P:interferon-gamma biosynthesis; IDA.
CC GO; GO:0042104; P:positive regulation of activated T-cell pro. .; ISS.
CC InterPro; IPR008996; Cytok_IL1_like.
KW Cytokine.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
FT SEQUENCE 193 AA; 22037 MW; 0D973B586F461F25 CRC64;
Query Match 75.5%; Score 613; DB 1; Length 193;
Best Local Similarity 73.7%; Pred. No. 3.5e-50;
Matches 115; Conservative 23; Mismatches 18; Indels 0; Gaps 0;
QY 1 YFGKLEKSLVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 37 YFGKLEKSLVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSLTRL 96
QY 61 AVTISVKCEKISLSCENKILSFEMPPDNKTKSDIIFQSVPGHDKMOPFESSY 120
Db 97 AVTISVKYKNTSLSCNKLTISFQMSPPDSINDEGNDIIFQSVPGHDDKIQFESSLY 156
QY 121 EGYFLACEKERDLFKLILKKEDELDGDRSIMFTVQNE 156
Db 157 KGHFLACKCKENDLFKILKDKDENGKDSIMFTVQNK 192
RESULT 6
IL18 MOUSE STANDARD; PRT; 192 AA.
AC P70380;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor).
DE (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX TISSUE=Liver;
RC MEDLINE=96061009; PubMed=7477296;
RA Okamura H., Tsutsumi H., Komatsu T., Yutsudo M., Hakura A.,

```

```

RA Tanimoto T., Torigoe K., Okura T., Mukada Y., Hattori K.,
RA Akita K., Namba M., Tanabe F., Konishi K., Fukuda S., Kurimoto M.;
RT "Cloning of a new cytokine that induces IFN-gamma production by T
RT cells.";
RN Nature 378:88-91(1995).
RP SEQUENCE OF 1-191 FROM N.A.
RX STRAIN=NOD; TISSUE=Pancreas;
RX MEDLINE=97174346; PubMed=9022080;
RA Rothe H., Jenkins N.A., Copeland N.G., Kolb H.;
RT "Active stage of autoimmune diabetes is associated with the
RT expression of a novel cytokine, IGIF, which is located near Idd2.";
RL J. Clin. Invest. 99:469-474(1997).
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-1 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D49949; BAA08705.1; -.
CC EMBL; U66244; AAB49753.1; -.
CC PIR; S60226; S60226.
CC MGD; MGI:107936; IL18.
CC GO; GO:0005576; C:extracellular; ISS.
CC GO; GO:0016506; F:apoptosis activator activity; TAS.
CC GO; GO:0005125; P:cytokine activity; ISS.
CC GO; GO:0001525; P:angiogenesis; ISS.
CC GO; GO:0042033; P:chemokine biosynthesis; ISS.
CC GO; GO:004253; P:granulocyte macrophage colony-stimulating f. .; ISS.
CC GO; GO:0008625; P:induction of apoptosis via death domain rec. .; TAS.
CC GO; GO:0042035; P:interferon-gamma biosynthesis; IMP.
CC GO; GO:004231; P:interleukin-13 biosynthesis; TAS.
CC GO; GO:0042094; P:interleukin-2 biosynthesis; ISS.
CC GO; GO:0042104; P:positive regulation of activated T-cell pro. .; ISS.
CC GO; GO:0030155; P:regulation of cell adhesion; ISS.
CC GO; GO:0030431; P:sleep; ISS.
CC InterPro; IPR008996; Cytok_IL1 like.
CC InterPro; IPR009075; Interleukin_1.
CC Pfam; PF00340; IL1; 1.
CC SMART; SM00125; IL1; 1.
KW Cytokine.
FT PROPEP 1 35
FT CHAIN 36 192 INTERLEUKIN-18.
FT CONFLICT 183 185 MFT -> IS (IN REF. 2).
SQ SEQUENCE 192 AA; 22135 MW; 8FED938473874D63 CRC64;
Query Match 63.4%; Score 515; DB 1; Length 192;
Best Local Similarity 64.9%; Pred. No. 4.7e-41;
Matches 100; Conservative 27; Mismatches 25; Indels 2; Gaps 2;
QY 2 FGKLEKSLVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGMA 61
Db 37 FGRLLHCTTAVIRNLNDQVLFVDK-RQPVFEDMTDIDQASASEPQTRLLIYMYKDSVVRGLA 95
QY 62 VTISVKCEKISLSCENKILSFEMPPDNKTKSDIIFQSVPGHDKMOPFESSY 121
Db 96 VTISVKDSRMTSLSCNKLTISFEMDPENIDDIQSDLIFFQKRVPGH-NRMEFESSLYE 154
QY 122 GYFLACEKERDLFKLILKKEDELDGDRSIMFTVQNK 155
Db 155 GHFLACQKEDAFKILKDKDENGKDSVMTFLIN 188
RESULT 7
IL18 RAT

```

ID IL18 RAT STANDARD; PRT; 194 AA.  
 AC P97636; O88749; P97637;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)  
 DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).  
 GN IL18 OR IGIF.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RN SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
 RC STRAIN=Sprague-Dawley; TISSUE=Adrenal gland;  
 RX MEDLINE=97152963; PubMed=8998986;  
 RA Culhane A.C., Hall M.D., Rothwell N.J., Lusheshi G.N.;  
 RT "Cloning of rat brain interleukin-18 cDNA";  
 RL Mol. Psych. 3:362-366(1998).  
 CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS  
 CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I  
 CC CELLS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=Beta;  
 CC Name=Alpha;  
 CC IsoId=P97636-1; Sequence=Displayed;  
 CC IsoId=P97636-2; Sequence=VSP\_002659;  
 CC -1- SIMILARITY: Belongs to the IL-1 family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; U77776; AAC53009.1; -;  
 CC EMBL; U77777; AAC53010.1; -;  
 CC EMBL; AJ222813; CAA11001.1; -;  
 CC GO; GO:0005576; C:extracellular; ISS.  
 CC GO; GO:0016506; P:apoptosis activator activity; ISS.  
 CC GO; GO:0005125; P:cytokine activity; ISS.  
 CC GO; GO:0005125; P:angiogenesis; ISS.  
 CC GO; GO:0008625; P:induction of apoptosis via death domain rec. .; ISS.  
 CC GO; GO:0042095; P:interferon-gamma biosynthesis; ISS.  
 CC GO; GO:0042104; P:positive regulation of activated T-cell pro. .; ISS.  
 CC GO; GO:0030155; P:regulation of cell adhesion; ISS.  
 CC GO; GO:0045188; P:regulation of non-REM sleep; TAS.  
 CC GO; GO:0030431; P:sleep; IDA.  
 CC InterPro; IPR008996; Cytok IL1 like.  
 CC InterPro; IPR000975; Interleukin\_1.  
 CC Pfam; PF00340; IL1; 1.  
 CC SMART; SM00125; IL1; 1.  
 CC Cytokine; Alternative splicing.  
 CC PROPEP 1 36  
 CC CHAIN 37 194  
 CC VARSPLIC 121 139  
 CC /FTID=VSP\_002659.  
 CC CONFLICT 4 5  
 CC CONFLICT 48 48 MS -> IP (IN REF. 2).  
 CC CONFLICT 1 1 I -> M (IN REF. 2).  
 CC SEQUENCE 194 AA; 22303 MW; E2089AD6F1798450 CRC64;

Query Match 63.4%; Score 514.5; DB 1; Length 194;  
 Best Local Similarity 63.2%; Pred. No. 5.3e-41;  
 Matches 98; Conservative 28; Mismatches 28; Indels 1; Gaps 1;  
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLPFDMDTSDCRDNPARTIFITISMYKDSQPRGM 60  
 DB 37 HFGRLHCTTAVIRSLNDQVLFVDKRNPFVDFMDPDIDRTANESQTRLLIYYKDSVEVKGL 96  
 QY 61 AVTISVKEKISXLSKCNKIISFKEMPPDNKIDTKSDIIFQFORSVPGHDKMKNQFESSY 120  
 DB 97 AVTILSVKDGSRMSTLCKNKIISPEMNPENIDDKSLIFFQKRVPGH-NKMEFESSLY 155  
 QY 121 EGYELACEKEDLEFKLLKKDELGDRSIMPTVQN 155  
 DB 156 EGHFLACQKEDDAFKLVLRKRDENGKSVMPFTLN 190  
 RESULT 8  
 IL18 CHICK  
 ID IL18 CHICK STANDARD; PRT; 196 AA.  
 AC Q8QFQ8;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Interleukin-18 precursor (IL-18).  
 GN IL18.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RA Rothwell L., Buerstedde J.M., Kaiser P.;  
 RT "Cloning and characterisation of chicken interleukin-18";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS  
 CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I  
 CC CELLS (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -1- SIMILARITY: Belongs to the IL-1 family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; AJ276025; CAC81652.1; -;  
 CC InterPro; IPR008996; Cytok IL1 like.  
 CC PROPEP 1 29  
 CC CHAIN 30 196  
 CC SEQUENCE 196 AA; 22787 MW; 4947DECCB92414 CRC64;  
 Query Match 22.0%; Score 178.5; DB 1; Length 196;  
 Best Local Similarity 34.3%; Pred. No. 1.1e-09;  
 Matches 60; Conservative 26; Mismatches 68; Indels 21; Gaps 8;  
 QY 1 YFGKLESKL-----SVIRNLNDQVLFIDQGNRPLPFDMDTSDCRDNPARTIFITISM 51  
 DB 20 YFELECDAPCKDKTKIRFRFNVNSQLLVVRPLNVAFAFEDVTDQEVKGS-GMYFDIHC 78  
 QY 52 YKDSQPRG-MAYTISVKCEKISXLSCKN-----IISFKEMPPDNKIDTKSDIIFQFORS 105  
 DB 79 YKTAPSARMPAFVSQVQEDKSYMCCEKHGKQMVFRFGEVPGKDPFG-ESNIIFFKKT 137  
 QY 106 VPGHDKN-MQFESSSYEGYFLACEKERDLFKLKK-----EDELGDRSIMPTVQNE 156  
 DB 138 FTSCSKAFKFEYSLEQGMFLAFEEEDSLRKLKLLKPREDEVDVETTKFTVTSNE 192

```

RESULT 9
FAT2_DROME
ID FAT2_DROME STANDARD; PRT; 4705 AA.
AC Q9VW71; Q95S51;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Putative fat-like cadherin-related tumor suppressor homolog
DE precursor.
GN FAT2 OR CG7749.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foslter A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glöckner A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kianos I., Simpson M., Skupski M.F., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP REVISIONS.
RX MEDLINE=22426069; PubMed=12537572;
RA Mira S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.N., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [3]
RP SEQUENCE OF 3837-4705 FROM N.A.

```

---

```

RC STRAIN=Berkeley; TISSUE=Ovary;
RX MEDLINE=22426066; PubMed=12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA George R.A., Guarin H., Krommiller B., Pacleb J.M., Park S., Wan K.H.,
RA Rubin G.M., Celniker S.E.;
RT "A Drosophila full-length cDNA resource.";
RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- SIMILARITY: Contains 34 cadherin domains.
CC -!- SIMILARITY: Contains 5 EGF-like domains.
CC -!- SIMILARITY: Contains 1 laminin G-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE003515; AAF49078.2; -;
CC EMBL; AY060955; AAL28503.1; ALT_INIT.
CC EMBL; AY118666; AAM50035.1; ALT_INIT.
CC HSSP; P15116; INCI.
CC FlyBase; FBgn0036930; fat2.
CC GO; GO:0005887; C:integral to plasma membrane; ISS.
CC GO; GO:0008014; F:calcium-dependent cell adhesion molecule ac. .; ISS.
CC GO; GO:0016339; P:calcium-dependent cell-cell adhesion; ISS.
CC InterPro; IPR000152; ASX_hydroxyl_S.
CC InterPro; IPR002126; Cadherin.
CC InterPro; IPR008985; Cona like lec_gf.
CC InterPro; IPR001881; EGF Ca.
CC InterPro; IPR006209; EGF like.
CC InterPro; IPR006210; IEGF.
CC InterPro; IPR001791; Laminin G.
CC Pfam; PF000028; cadherin; 31.
CC Pfam; PF00054; laminin G; 1.
CC PRINTS; PR00205; CADHERIN.
CC SMART; SM00112; CA; 34.
CC SMART; SM00181; EGF; 6.
CC SMART; SM00282; LamG; 1.
CC PROSITE; PS00010; ASX HYDROXYL; 1.
CC PROSITE; PS00232; CADHERIN 1; 18.
CC PROSITE; PS0268; CADHERIN 2; 34.
CC PROSITE; PS00022; EGF 1; 5.
CC PROSITE; PS01186; EGF 2; 2.
CC PROSITE; PS00026; EGF 3; 5.
CC PROSITE; PS01187; EGF CA; 1.
CC PROSITE; PS00025; LAM G DOMAIN; 1.
KW Hypothetical protein; Cell adhesion; Signal; Glycoprotein;
KW Transmembrane; Calcium; Calcium-binding; Repeat; EGF-like domain.
FT SIGNAL 1 35
FT CHAIN 36 4705
FT PUTATIVE FAT-LIKE CADHERIN-RELATED TUMOR
FT SUPPRESSOR HOMOLOG.
FT EXTRACELLULAR (POTENTIAL).
FT CYTOPLASMIC (POTENTIAL).
FT CADHERIN 1.
FT CADHERIN 2.
FT CADHERIN 3.
FT CADHERIN 4.
FT CADHERIN 5.
FT CADHERIN 6.
FT CADHERIN 7.
FT CADHERIN 8.
FT CADHERIN 9.
FT CADHERIN 10.
FT CADHERIN 11.
FT CADHERIN 12.
FT CADHERIN 13.
FT CADHERIN 14.
FT CADHERIN 15.

```

```

FT DOMAIN 1715 1812 CADHERIN 16.
FT DOMAIN 1813 1929 CADHERIN 17.
FT DOMAIN 1930 2030 CADHERIN 18.
FT DOMAIN 2031 2137 CADHERIN 19.
FT DOMAIN 2138 2238 CADHERIN 20.
FT DOMAIN 2239 2338 CADHERIN 21.
FT DOMAIN 2339 2465 CADHERIN 22.
FT DOMAIN 2466 2567 CADHERIN 23.
FT DOMAIN 2568 2670 CADHERIN 24.
FT DOMAIN 2671 2779 CADHERIN 25.
FT DOMAIN 2780 2876 CADHERIN 26.
FT DOMAIN 2877 2983 CADHERIN 27.
FT DOMAIN 2984 3088 CADHERIN 28.
FT DOMAIN 3084 3185 CADHERIN 29.
FT DOMAIN 3186 3289 CADHERIN 30.
FT DOMAIN 3290 3394 CADHERIN 31.
FT DOMAIN 3395 3499 CADHERIN 32.
FT DOMAIN 3500 3604 CADHERIN 33.
FT DOMAIN 3605 3712 CADHERIN 34.
FT DOMAIN 3819 3879 EGF-LIKE 1.
FT DOMAIN 3881 3919 EGF-LIKE 2.
FT DOMAIN 3937 4121 LAMININ G-LIKE.
FT DOMAIN 4129 4166 EGF-LIKE 3.
FT DOMAIN 4168 4205 EGF-LIKE 4.
FT DOMAIN 4243 4279 EGF-LIKE 5.
FT DISULFID 3823 3835 POTENTIAL.
FT DISULFID 3830 3867 POTENTIAL.
FT DISULFID 3869 3878 POTENTIAL.
FT DISULFID 3885 3896 POTENTIAL.
FT DISULFID 3890 3907 POTENTIAL.
FT DISULFID 3909 3918 POTENTIAL.
FT DISULFID 4133 4144 POTENTIAL.
FT DISULFID 4138 4154 POTENTIAL.
FT DISULFID 4156 4165 POTENTIAL.
FT DISULFID 4172 4183 POTENTIAL.
FT DISULFID 4177 4193 POTENTIAL.
FT DISULFID 4195 4204 POTENTIAL.
FT DISULFID 4247 4258 POTENTIAL.
FT DISULFID 4252 4267 POTENTIAL.
FT DISULFID 4269 4278 POTENTIAL.
FT CARBOHYD 65 65 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 364 364 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 779 779 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 843 843 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 923 923 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1106 1106 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1198 1198 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1312 1312 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1439 1439 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1473 1473 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1511 1511 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 3962 3962 G -> E (IN REF. 3; AAL28503).
SQ SEQUENCE 4705 AA; 524564 MW; 6D387A489D2C33DE CRC64;

Query Match 10.8%; Score 88; DB 1; Length 4705;
Best Local Similarity 23.6%; Pred. No. 13;
Matches 38; Conservative 25; Mismatches 56; Indels 42; Gaps 7;

QY 32 DMTDSDCRNAPRTIFITISMY---KDSQGRGMATVTSVKCEKISLSCENKIISF--KE 85
Db 2124 DISVLVDNDCP--LFVNMPIYATVSDIDPKG---TIIIMQKALDLSAENGVEYELKK 2178
QY 86 MNPDPNIDKTDKSDIIFQRSVPGHDKMKQPESSYEGYFLACEKRDL-----133
Db 2179 NGGEFLKLRKSGELSIKQHVGEHNRNVELTVAAYDGAITPCSSEAPLQVKVIDRSMPEV 2238
QY 134 ---FKLILKED-----ELGDRSTMFTVQNE 156
Db 2239 EKQFYTVSVKREDVEMYGALSIVSIEAESPLG-RSLIYTISSSE 2278

RESULT 10

```

```

IL1A_PIG
ID IL1A_PIG STANDARD; PRT; 270 AA.
AC P18430;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Interleukin-1 alpha precursor (IL-1 alpha).
GN IL1A.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=90332454; PubMed=2377484;
RA Maliszewski C.R., Renshaw B.R., Schoenborn M.A., Urban J.F.,
RA Baker P.E.;
RT "Porcine IL-1 alpha cDNA nucleotide sequence.";
RL Nucleic Acids Res. 18:4282-4282(1990).
[2]
RP SEQUENCE FROM N.A.
RA Huether M.J., Scamurra R.W., Murtaugh M.P., Molitor T.W.;
RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
CC -|- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE. B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -|- SUBUNIT: Monomer.
CC -|- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -|- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -|- SIMILARITY: Belongs to the IL-1 family.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; X52731; CAA36945.1; -.
DR EMBL; M86730; AAA73198.1; -.
DR PIR; I46620; I46620.
DR PIR; S10532; S10532.
DR HSP; P01583; IITA.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR003502; IL1_propep.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR Pfam; PF02394; IL1_propep; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN 1; 1.
DR SMART; SM00125; IL1; 1.
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 112
FT CHAIN 113 270 INTERLEUKIN-1 ALPHA.
FT CARBOHYD 102 102 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 89 89 N -> I (IN REF. 2).
FT CONFLICT 242 242 F -> L (IN REF. 2).
FT CONFLICT 255 255 P -> R (IN REF. 2).
SQ SEQUENCE 270 AA; 30788 MW; 5677BF2B0EF63839 CRC64;

Query Match 10.0%; Score 81.5; DB 1; Length 270;
Best Local Similarity 22.7%; Pred. No. 1.7;
Matches 30; Conservative 32; Mismatches 57; Indels 13; Gaps 6;

```



[illegible]

```

DP03_CLOPE
ID_DP03_CLOPE STANDARD; PRT; 1449 AA.
AC Q8XJR3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA polymerase III polC-type [EC 2.7.7.7] (PolIII).
GN POLC OR CPFL691.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OC NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayaehi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
CC CC -1- FUNCTION: Required for replicative DNA synthesis. This DNA
CC polymerase also exhibits 3' to 5' exonuclease activity (By
CC similarity).
CC CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + {DNA}(n).
CC CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC CC -1- SIMILARITY: Belongs to the DNA polymerase type-C family. PolC
CC subfamily.

```

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See [http://www.isb-sib.ch/announce/entire\\_send\\_an\\_email\\_to\\_license@isb-sib.ch](http://www.isb-sib.ch/announce/entire_send_an_email_to_license@isb-sib.ch)).

ENBL1; AF0003191; BAB81397.1; -	DR
HAMAP; MF 00356; -; 1.	DR
InterPro; IPR006054; DnaQ.	DR
InterPro; IPR006055; Exonuclease	DR
InterPro; IPR004013; PHP C.	DR
InterPro; IPR003141; PHP C.	DR
InterPro; IPR006308; PolC gram	DR
Pfam; PF00929; Exonuclease; 1.	DR
Pfam; PF02811; PHP C; 1.	DR
Pfam; PF02231; PHP N; 1.	DR
SMART; SM00479; EXOIII; 1.	DR
SMART; SM00481; POLIIIac; 1.	DR
TIGRfams; TIGR00573; dnaq; 1.	DR
TIGRfams; TIGR01405; polC gram	DR
Transferase; DNA-directed DNA	DR
Nuclease; Exonuclease; complet	DR





Best Local Similarity 22.3%; Pred. No. 5;  
Matches 29; Conservative 28; Mismatches 62; Indels 11; Gaps 4;  
QY 7 SKLSVIRNLNDQVLFIDQGNRPFLPDMTDSDCRDNPRTI-----FIISMVYKDSQPRGMA 61  
Db 122 TRYPMRIVNHQCTINDALNOSVIRDTSGQVLAALNNLDDAVKFDMGAYTSEDSQLP 181  
QY 62 VTISV-KCEKISXLSCEKNIISFKEM-NPPDNIKDKTSIIFFQRSVFGHDKMKQFFESS 119  
Db 182 VTLRISKTRLFVSAQNEDEPVLKEMPTPKTIKDETLLFEWER-----HGSKNYFKSVA 237  
QY 120 YEGYFLACEK 129  
Db 238 HPKLFIAATKQ 247  
Search completed: August 19, 2004, 13:35:28  
Job time : 14 secs

606 ETVEVKYINKIASMSCRAAVKANDVLSILEMENLIEDLRYINDPFCPHGRPTIIFK 661  
Db IL1A\_HORSE STANDARD; PRT; 270 AA.  
RESULT 15  
ID IL1A\_HORSE AC Q28385; 077743; PRT; 270 AA.  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Interleukin-1 alpha precursor (IL-1 alpha).  
GN IL1A.  
OS Equus caballus (Horse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_TaxID=9796;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96131982; PubMed=8578682;  
RA Kato H., Ohashi T., Nakamura N., Nishimura Y., Watari T., Goitsuka R.,  
RA Tsujimoto H., Hasegawa A.;  
RT "Molecular cloning of equine interleukin-1 alpha and -beta cDNAs.";  
RL Vet. Immunol. Immunopathol. 48:221-231(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98285941; PubMed=9622738;  
RA Howard R.D., McIlwraith C.W., Trotter G.W., Nyborg J.K.;  
RT "Cloning of equine interleukin-1 alpha and equine interleukin-1 beta  
and determination of their full-length cDNA sequences.";  
RL Am. J. Vet. Res. 59:704-711(1998).  
CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES  
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL  
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.  
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING  
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE  
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS  
CC (BY SIMILARITY).  
CC -!- SUBUNIT: Monomer (By similarity).  
CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE  
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.  
CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE  
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS  
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER  
CC SECRETORY PROTEINS.  
CC -!- SIMILARITY: Belongs to the IL-1 family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; D42146; BAA07717.1; -;  
CC EMBL; U92480; AAC39255.1; -;  
CC HSP; P01583; LITA.  
CC InterPro; IPR008996; Cytok\_III\_like.  
CC InterPro; IPR003502; IL1\_propep.  
CC InterPro; IPR000975; Interleukin\_1.  
CC Pfam; PF00340; IL1; 1.  
CC Pfam; PF02394; IL1\_propep; 1.  
CC SMART; SM00125; IL1; 1.  
CC PROSITE; PS00253; INTERLEUKIN\_1; 1.  
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.  
FT PROPEP 1 112 BY SIMILARITY.  
FT CHAIN 113 270 INTERLEUKIN-1 ALPHA.  
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 110 110 R -> K (IN REF. 2).  
FT CONFLICT 150 150 G -> V (IN REF. 2).  
SQ SEQUENCE 270 AA; 30806 MW; 381859713754DE90 CRC64;

Query Match . 9.4%; Score 76.5; DB 1; Length 270;

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2004, 13:32:15 ; Search time 39 Seconds

(without alignments)  
1270.163 Million cell updates/sec

Title: US-09-716-356A-6

Perfect score: 812

Sequence: 1 YFGKLSKLSVIRNLNDQVL.....LKKEDLGDRSIMFTVQNE 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25.\*

1: sp\_archea.\*

2: sp\_bacteria.\*

3: sp\_fungi.\*

4: sp\_human.\*

5: sp\_invertebrate.\*

6: sp\_mammal.\*

7: sp\_mhc.\*

8: sp\_organelle.\*

9: sp\_phase.\*

10: sp\_plant.\*

11: sp\_rodent.\*

12: sp\_virus.\*

13: sp\_vertebrate.\*

14: sp\_unclassified.\*

15: sp\_rvirus.\*

16: sp\_bacteriap.\*

17: sp\_archeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	798	98.3	193	4	Q96KJ8
2	792	97.5	193	6	Q9BG15
3	654	80.5	178	6	Q9MZL8
4	648	79.8	193	6	Q9GL09
5	634	78.1	192	6	Q95W33
6	633	78.0	192	6	Q95B38
7	626	77.1	192	6	Q9N1P7
8	536.5	66.1	195	11	Q80Y07
9	515	63.4	189	11	Q80SS8
10	441	54.3	196	11	Q91Z66
11	313	38.5	84	6	Q95LE7
12	204	25.1	45	4	Q9NQ49
13	193	23.8	211	13	Q98SQ1
14	184.5	22.7	198	13	Q8AV26
15	182.5	22.5	198	13	Q918D2
16	86.5	10.7	376	11	Q8K4E7

17	86.5	10.7	376	11	Q8K4E6	Q8k4e6 mus musculu
18	85	10.5	252	11	Q8JZN4	Q8jzn4 mus musculu
19	85	10.5	381	3	O43031	O43031 schizosacch
20	84.5	10.4	376	11	Q8K4E8	Q8k4e8 mus musculu
21	83.5	10.3	454	6	Q8HZU7	Q8hzu7 tonatia sau
22	83.5	10.3	454	6	Q8HZU6	Q8hzu6 tonatia sau
23	83.5	10.3	454	6	Q8HZU5	Q8hzu5 tonatia sau
24	83	10.2	376	11	Q8JZN0	Q8jzn0 mus musculu
25	82.5	10.2	268	6	Q865X7	Q865x7 lama glama
26	82	10.1	263	3	O74316	O74316 schizosacch
27	82	10.1	1534	5	Q8MPV7	Q8mpv7 caenorhabdi
28	81.5	10.0	599	5	Q8I2G6	Q8i2g6 plasmodium
29	81.5	10.0	617	5	Q25986	Q25986 plasmodium
30	81.5	10.0	1049	2	Q93KF0	Q93kf0 caldicellul
31	80.5	9.9	825	5	Q8IC17	Q8ic17 plasmodium
32	80.5	9.9	866	16	O84500	O84500 chlamydia t
33	79.5	9.8	595	10	Q9SDM4	Q9sdm4 dunaliella
34	79.5	9.8	1044	3	O94173	O94173 pneumocysti
35	79	9.7	452	16	O25249	O25249 helicobacte
36	79	9.7	10578	5	Q8ISF5	Q8isf5 caenorhabdi
37	79	9.7	18519	5	Q8ISF6	Q8isf6 caenorhabdi
38	79	9.7	18534	5	Q8ISF7	Q8isf7 caenorhabdi
39	78.5	9.7	204	2	Q9ZNF7	Q9znf7 clostridium
40	78.5	9.7	1061	16	Q8DU02	Q8du02 streptococc
41	78	9.6	261	16	Q8CU21	Q8cu21 streptococc
42	78	9.6	277	16	Q8DU44	Q8du44 streptococc
43	78	9.6	473	5	O16673	O16673 caenorhabdi
44	78	9.6	2578	5	Q8IJP9	Q8ijp9 plasmodium
45	77.5	9.5	454	6	Q8HZU4	Q8hzu4 tonatia bid

## ALIGNMENTS

RESULT 1

Q96KJ8 ID Q96KJ8 PRELIMINARY; PRT; 193 AA.  
AC Q96KJ8  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Interleukin 18.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ying P., Jianxin L.;  
RT "Cloning of Mutant Human Interleukin 18 cDNA."  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF380360; AAK57024.1; -  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR008996; Cytok\_III-like.  
DR InterPro; IPR000975; Interleukin\_1.  
DR SMART; SMO0125; IL1; 1.  
SQ SEQUENCE 193 AA; 22323 MW; 2E500205D1B7E5F7 CRC64;

Query Match 98.3%; Score 798; DB 4; Length 193;

Best Local Similarity 97.5%; Pred. NO. 2.7e-71;

Matches 153; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YFGKLSKLSVIRNLNDQVLFDQGNRPFDFTDSDCRDNAPRTIFISMYKDSQPRGM 60

Db 37 YFGKLSKLSVIRNLNDQVLFDQGNRPFDFTDSDCRDNAPRTIFISMYKDSQPRGM 96

QY 61 AVTISVKCKISXLSCKNIISFKEMNPPDNIKDTKSDIIFQSVFGHDKNQKFESSY 120

Db 97 AVTISVKCKISXLSCKNIISFKEMNPPDNIKDTKSDIIFQSVFGHDKNQKFESSY 156

QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157



DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Interferon-gamma inducing factor.  
GN IGIF.  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI\_TaxID=9685;  
[1]  
RN SEQUENCE FROM N.A.  
RA Hanlon L., McGillivray C.P., Argyle D.J.A., Nicolson L., Onions D.E.;  
RT "Nucleotide sequence of feline IGIF cDNA (provisional).";  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Y13923; CAC42918.1; -.  
DR InterPro; IPR008996; Cytok\_IL1\_like.  
SQ SEQUENCE 192 AA; 22068 MW; 5878C3DAC7A43358 CRC64;  
  
Query Match 78.1%; Score 634; DB 6; Length 192;  
Best Local Similarity 76.4%; Pred. No. 5.1e-55;  
Matches 120; Conservative 21; Mismatches 16; Indels 0; Gaps 0;  
  
Qy 1 YFGKLEKSLVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 60  
Db 36 YFGKLEKSLVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 95  
Qy 61 AVTISVCKEKLXSLSCENKIISFKEMPPDNKDTKSDIIFQSRVFGHDNMKFESSY 120  
Db 96 AVTISVNYKMTSLSCENKIISFKEMSPPEINDEGNDIIFQSRVFGHDNMKFESSY 155  
Qy 121 EGYFLACEKRDLPFLILKKDELDGDRSIMFTVQNE 157  
Db 156 KGYPFLACEKRDLPFLILKKDELDGDRSIMFTVQNK 192  
  
RESULT 6  
ID Q865B8 PRELIMINARY; PRT; 192 AA.  
AC Q865B8;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Interferon gamma inducing factor precursor.  
GN FIU-18.  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI\_TaxID=9685;  
[1]  
RN SEQUENCE FROM N.A.  
RA Kuwahara C., Kawakami K., Kishi M., Mochizuki M.;  
RT "Feline interleukin-18.";  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB056857; BAC65243.1; -.  
DR InterPro; IPR008996; Cytok\_IL1\_like.  
KW Signal.  
FT SIGNAL 1 35 Potential.  
SQ SEQUENCE 192 AA; 22071 MW; 204F32D131588513 CRC64;  
  
Query Match 78.0%; Score 633; DB 6; Length 192;  
Best Local Similarity 76.9%; Pred. No. 6.4e-55;  
Matches 120; Conservative 20; Mismatches 16; Indels 0; Gaps 0;  
  
Qy 1 YFGKLEKSLVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 60  
Db 36 YFGKLEKSLVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 95  
Qy 61 AVTISVCKEKLXSLSCENKIISFKEMPPDNKDTKSDIIFQSRVFGHDNMKFESSY 120  
Db 96 AVTISVNYKMTSLSCENKIISFKEMSPPEINDEGNDIIFQSRVFGHDNMKFESSY 155  
Qy 121 EGYFLACEKRDLPFLILKKDELDGDRSIMFTVQNE 156  
Db 156 KGYPFLACEKRDLPFLILKKDELDGDRSIMFTVQNK 192

Db 156 KGYPFLACEKRDLPFLILKKDELDGDRSIMFTVQNK 191  
  
RESULT 7  
ID Q9N1P7 PRELIMINARY; PRT; 192 AA.  
AC Q9N1P7;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Interleukin-18.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
[1]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Lung.  
RC MEDLINE=20356335; PubMed=10901174;  
RX Oem J.K., Song H.J., Kang S.W., Jeong W.S.;  
RA "Cloning, sequencing, and expression of porcine interleukin-18 in Escherichia coli.";  
RL Mol. Cells 10:343-347(2000).  
DR EMBL; AF176949; AAF35169.1; -.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR008996; Cytok\_IL1\_like.  
DR InterPro; IPR000975; Interleukin\_1.  
DR SMART; SMO0125; IL1; 1.  
SQ SEQUENCE 192 AA; 21969 MW; A51EB7A4E221A16D CRC64;  
  
Query Match 77.1%; Score 626; DB 6; Length 192;  
Best Local Similarity 73.9%; Pred. No. 3.2e-54;  
Matches 116; Conservative 25; Mismatches 16; Indels 0; Gaps 0;  
  
Qy 1 YFGKLEKSLVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 60  
Db 36 YFGKLEKSLVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 95  
Qy 61 AVTISVCKEKLXSLSCENKIISFKEMPPDNKDTKSDIIFQSRVFGHDNMKFESSY 120  
Db 96 AVTISVQCKWMTSLSCNKTLISFKEMSPPEINDEGNDIIFQSRVFGHDNMKFESSY 155  
Qy 121 EGYFLACEKRDLPFLILKKDELDGDRSIMFTVQNE 157  
Db 156 KGYPFLACEKRDLPFLILKKDELDGDRSIMFTVQSKN 192  
  
RESULT 8  
ID Q80Y07 PRELIMINARY; PRT; 195 AA.  
AC Q80Y07;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Interleukin 18.  
GN IL18.  
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;  
OC Meriones.  
OX NCBI\_TaxID=10047;  
[1]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Peritoneum;  
RC MEDLINE=22593022; PubMed=12706898;  
RX Gaucher D., Chadee K.;  
RT "Gerbil interleukin-18 and caspase-1: cloning, expression and characterization.";  
RL Gene 307:159-166(2003).  
DR EMBL; AY095932; AAM34434.1; -.  
DR InterPro; IPR008996; Cytok\_IL1\_like.

```
SQ SEQUENCE 195 AA; 22172 MW; C6P815317953154D CRC64;

Query Match 66.1%; Score 536.5; DB 11; Length 195;
Best Local Similarity 65.8%; Pred. No. 2.5e-45;
Matches 100; Conservative 29; Mismatches 22; Indels 1; Gaps 1;

QY 2 FGLKSLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYKDSOPRGMA 61
DB 39 FGLKSLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYKDSOPRGMA 98
QY 62 VTISVCKEIKSLSCENKIISFKEMNPPDNIDKTSDIIFQFORSVPGHDKNMQFESSSYE 121
DB 99 VTLVKDQTTMATLSCNKKIISFEEMPPENIDTSDLIFFQKRVPGH-NKMKFESSLYK 157

QY 122 GYFLACEKERDLFKLILKKEDELGRSIMFTVQN 153
DB 158 GHFLACQKEDDAFKLILKKEDELGRSIVMFTV 189

RESULT 9
Q9CS88 PRELIMINARY; PRT; 189 AA.
ID Q80SS8
AC Q80SS8;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Interleukin 18.
GN IL18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=B10.S/DvTe, and SUL/J; TISSUE=Spleen;
RA Gao J., Teuscher C.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY157834; AAO21309.1; -
DR EMBL; AY157835; AAO21310.1; -
DR InterPro; IPR008996; Cytok_IL1_like.
SQ SEQUENCE 189 AA; 21862 MW; E8F9E5EC01864665 CRC64;

Query Match 63.4%; Score 515; DB 11; Length 189;
Best Local Similarity 64.9%; Pred. No. 3.2e-43;
Matches 100; Conservative 27; Mismatches 25; Indels 2; Gaps 2;

QY 2 FGLKSLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYKDSOPRGMA 61
DB 34 FGRLHCTTAVIRNNDQVLFVDK-RQVFEDMTDIDQSASEPQTRLIITYMYKDSVVRGLA 92
QY 62 VTISVCKEIKSLSCENKIISFKEMNPPDNIDKTSDIIFQFORSVPGHDKNMQFESSSYE 121
DB 93 VTLVSKDSKSTLSCNKKIISFEEMPPENIDQSDLIFFQKRVPGH-NKMEFESSLYE 151

QY 122 GYFLACEKERDLFKLILKKEDELGRSIMFTVQN 155
DB 152 GHFLACQKEDDAFKLILKKEDELGRSIVMFTLN 185

RESULT 10
Q91Z66 PRELIMINARY; PRT; 196 AA.
ID Q91Z66;
AC Q91Z66;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Interleukin 18.
GN IL18.
OS Sigmodon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmodon.
OX NCBI_TaxID=42415;
```

```
[1]
RN SEQUENCE FROM N.A.
RP Blanco J.C., Pletneva L.M., Prince G.A.;
RT "Sigmodon hispidus cytokines, chemokines and interferons.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY059406; AAL26703.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005149; P:interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR008996; Cytok_IL1_like.
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 196 AA; 22545 MW; E27C5BDC397F951C CRC64;

Query Match 54.3%; Score 441; DB 11; Length 196;
Best Local Similarity 59.4%; Pred. No. 7.5e-36;
Matches 92; Conservative 24; Mismatches 37; Indels 2; Gaps 2;

QY 2 FGLKSLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYK-DSOPRGM 60
DB 39 FFKESSTTAVIRNNDYVLFIDREKSPVFEDMPADQKANEATRLIITYMYKDFNPGGL 98
QY 61 AVTISVCKEIKSLSCENKIISFKEMNPPDNIDKTSDIIFQFORSVPGHDKNMQFESSY 120
DB 99 PVTLSVRDRTMRTLSCNKKIISFEEMDPPLDGTGKSDLIFFQRAVPGH-NKMKFESSLH 157

QY 121 EGYFLACEKERDLFKLILKKEDELGRSIMFTVQN 155
DB 158 EGHFLACRDRGDSFKLILKKEDELGRSIVMFTV 192

RESULT 11
Q95LE7 PRELIMINARY; PRT; 84 AA.
ID Q95LE7;
AC Q95LE7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE IL-18 (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Chamizo C., Rubio J.M., Moreno J., Alvar J.;
RT "Semi-quantification of canine cytokine expression by one tube RT-PCR.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF327900; AAL26920.1; -
DR InterPro; IPR008996; Cytok_IL1_like.
FT NON_TER 1 1
FT NON_TER 84 84
SQ SEQUENCE 84 AA; 9568 MW; 19BD9E27F336774B CRC64;

Query Match 38.5%; Score 313; DB 6; Length 84;
Best Local Similarity 74.7%; Pred. No. 1.5e-23;
Matches 59; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 1 YFGKLSKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYKDSOPRGM 60
DB 5 YFGKLEPKLSIIRNLNDQVLFVNEGQPVFEDMPDSDCTDNAPHTFIITYMYKDSLTRL 64
QY 61 AVTISVCKEIKSLSCENK 79
DB 65 AVTISVKYKTMSTLSCNKK 83

RESULT 12
Q9NQ49 PRELIMINARY; PRT; 45 AA.
ID Q9NQ49
AC Q9NQ49;
```

DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
 DE Interleukin-18 (Fragment).  
 GN IL-18.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Fathan A.J., Pravica V., Hutchinson I.V.;  
 RT "Identification of Human Interleukin-18 gene polymorphisms";  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL; AJ295724; CAC01436.1; -;  
 DR InterPro; IPR008996; Cytok\_IL1\_like.  
 FT NON TER 1  
 FT NON TER 45  
 FT NON TER 45  
 SQ SEQUENCE 45 AA; 5266 MW; DF3A626507E3D61A CRC64;

Query Match 25.1%; Score 204; DB 4; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-13;  
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YFGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTDSDCR 39  
 Db 7 YFGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTDSDCR 45

RESULT 13  
 Q98SQ1 PRELIMINARY; PRT; 211 AA.  
 AC Q98SQ1:  
 DT 01-JUN-2001 (TReMBLrel. 17, Created)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
 DE Interleukin-18 (Fragment).  
 GN IL-18.  
 OS Anas platyrhynchos (Domestic duck).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.  
 OX NCBI\_TaxID=8839;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Chan W.-S., Warr G.W., Middleton D.L., Lundquist M.L., Higgins D.A.;  
 RT "Anas platyrhynchos T-cell antigens, IL-18 gene";  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL; AF336122; AAK26322.1; -;  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR008996; Cytok\_IL1\_like.  
 DR InterPro; IPR000975; Interleukin\_1.  
 DR SMART; SM00125; IL1; 1.  
 FT NON TER 1  
 FT NON TER 1  
 SQ SEQUENCE 211 AA; 24541 MW; CA6FC63538211B2B CRC64;

Query Match 23.8%; Score 193; DB 13; Length 211;  
 Best Local Similarity 36.5%; Pred. No. 3.3e-11;  
 Matches 61; Conservative 29; Mismatches 63; Indels 14; Gaps 9;  
 Qy 2 FGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTIFIIISMYKDSQP-RG 59  
 Db 43 FSKETKTLFRNVNSQLVVRPLDNLMAAFEDVTDQEKMGSGWN-FCHCYKTTTTSAG 101  
 Qy 60 MAVTISVKCE-KISXLSCEK- - - - - IISFKEMNPPDNKDTKSDIIFQRSVPGHDK-M 113  
 Db 102 MPVAFSVRVEDKSYMCCEBHGKMWVRFRGEVFKDIPG-ESNIIFFKKTFTSYSSKAF 160  
 Qy 114 QFSSSYEGYFLACEKRDLPKILKK- - - - - EDELGDRS-INFTVONE 156  
 Db 161 KFEYSLRGRGFLAFEEEDSLRKLILKKLPREDEVDVETTKILTSHNE 207

RESULT 14  
 Q8AV26 PRELIMINARY; PRT; 198 AA.  
 AC Q8AV26;  
 DT 01-MAR-2003 (TReMBLrel. 23, Created)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
 DE Interleukin-18 precursor (Fragment).  
 GN IL-18.  
 OS Meleagris gallopavo (Common turkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.  
 OX NCBI\_TaxID=9103;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=22195503; PubMed=12206831;  
 RA Kaiser P.;  
 RT "Turkey and chicken interleukin-18 (IL18) share high sequence  
 RT identity, but have different polyadenylation sites in their 3' UTR";  
 RL Dev. Comp. Immunol. 26:681-687(2002).  
 DR EMBL; AJ312000; CAC83483.1; -;  
 DR InterPro; IPR008996; Cytok\_IL1\_like.  
 KW Signal.  
 FT NON TER 1  
 FT NON TER 28  
 FT SIGNAL <1  
 FT CHAIN 29 198 INTERLEUKIN-18.  
 SQ SEQUENCE 198 AA; 22967 MW; AID450BC7207BFAD CRC64;

Query Match 22.7%; Score 184.5; DB 13; Length 198;  
 Best Local Similarity 34.9%; Pred. No. 2.2e-10;  
 Matches 58; Conservative 30; Mismatches 65; Indels 13; Gaps 7;  
 Qy 2 FGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTIFIIISMYKDSQP-RG 59  
 Db 31 FCKEKTIKLFRNVNSQLVVRPLDNLMAAFEDVTDQEKMGSGW-GMYFDIHCYKTTAPSAG 89  
 Qy 60 MAVTISVKCEKISXLSCEK- - - - - IISFKEMNPPDNKDTKSDIIFQRSVPGHDK-M 113  
 Db 90 MPVAFSVQVEDKSYMCCEBHGKMWVRFRGEVFKDIPG-ESNIIFFKKTFTSCSKAF 148  
 Qy 114 QFSSSYEGYFLACEKRDLPKILKK- - - - - EDELGDRSINFTVONE 156  
 Db 149 KFEYSLRGRGFLAFEEEDSLRKLILKKLPREDEVDVETTKFVTSRNE 194

RESULT 15  
 Q918D2 PRELIMINARY; PRT; 198 AA.  
 AC Q918D2;  
 DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
 DE Interleukin 18.  
 GN Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=20508574; PubMed=11054275;  
 RA Schneider K., Puehler F., Baeuerle D., Elvers S., Staeheli P.,  
 RA Kaspers B., Weining K.C.;  
 RT "cDNA cloning of biologically active chicken Interleukin-18";  
 RL J. Interferon Cytokine Res. 20:879-883(2000).  
 DR EMBL; AJ277865; CAB96214.1; -;  
 DR InterPro; IPR008996; Cytok\_IL1\_like.  
 FT CHAIN 30 198 INTERLEUKIN 18.  
 SQ SEQUENCE 198 AA; 22918 MW; 29BB77DC3E3C6600 CRC64;

Query Match 22.5%; Score 182.5; DB 13; Length 198;





GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2004, 13:34:05 ; Search time 19 Seconds  
(without alignments)  
426.594 Million cell updates/sec

Title: US-09-716-356A-6  
Perfect score: 812  
Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKKEDELGDRESIMFTVQNE 157

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	811	99.9	157	4	US-08-982-285-4
2	811	99.9	157	4	US-09-700-609-1
3	811	99.9	157	4	US-09-398-412B-7
4	810	99.8	157	2	US-08-896-605A-6
5	810	99.8	157	2	US-08-896-501A-4
6	810	99.8	157	3	US-08-884-324-1
7	810	99.8	157	3	US-08-996-338-26
8	810	99.8	157	3	US-08-558-818-1
9	810	99.8	157	3	US-08-974-469A-1
10	810	99.8	157	3	US-08-832-180-1
11	810	99.8	157	3	US-08-832-198-6
12	810	99.8	157	4	US-09-819-902-6
13	810	99.8	157	4	US-09-752-510-6
14	810	99.8	157	4	US-09-711-899-1
15	810	99.8	157	4	US-09-556-972-26
16	810	99.8	157	4	US-09-649-063-1
17	810	99.8	157	2	US-08-896-605A-2
18	810	99.8	157	2	US-08-896-501A-2
19	810	99.8	157	3	US-08-832-180-9
20	801	99.6	157	4	US-08-982-285-6
21	792	97.5	157	4	US-09-597-576-2
22	791	97.4	157	4	US-08-982-285-7
23	791	97.4	157	4	US-08-982-285-8
24	782	96.3	157	4	US-08-982-285-11
25	781	96.2	157	4	US-08-982-285-9
26	772	95.1	157	4	US-08-982-285-12
27	771	95.0	157	4	US-08-982-285-10

28	613	75.5	179	4	US-09-445-724B-14	Sequence 14, Appl
29	613	75.5	193	4	US-09-445-724B-2	Sequence 2, Appl
30	613	75.5	193	4	US-09-445-724B-6	Sequence 6, Appl
31	517	63.7	157	4	US-08-982-285-13	Sequence 13, Appl
32	515	63.4	157	4	US-08-982-285-5	Sequence 5, Appl
33	515	63.4	157	4	US-09-700-609-2	Sequence 2, Appl
34	515	63.4	158	4	US-09-398-412B-8	Sequence 8, Appl
35	513	63.2	157	2	US-08-502-535B-2	Sequence 2, Appl
36	513	63.2	157	2	US-08-908-005A-2	Sequence 2, Appl
37	513	63.2	157	3	US-08-996-338-27	Sequence 27, Appl
38	513	63.2	157	3	US-08-558-818-7	Sequence 7, Appl
39	513	63.2	157	3	US-08-974-469A-7	Sequence 7, Appl
40	513	63.2	157	3	US-08-832-180-8	Sequence 8, Appl
41	513	63.2	157	3	US-08-832-198-11	Sequence 11, Appl
42	513	63.2	157	3	US-09-253-523-2	Sequence 2, Appl
43	513	63.2	157	3	US-09-251-911-2	Sequence 2, Appl
44	513	63.2	157	4	US-09-819-902-11	Sequence 11, Appl
45	513	63.2	157	4	US-09-752-510-11	Sequence 11, Appl

## ALIGNMENTS

RESULT 1  
US-08-982-285-4  
; Sequence 4, Application US/08982285  
; Patent No. 6476197  
; GENERAL INFORMATION:  
; APPLICANT: YAMAMOTO, Koza  
; APPLICANT: OKAMOTO, Iwao  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: POLYPEPTIDES  
; NUMBER OF SEQUENCES: 51  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 419 7th Street N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/982,285  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 333,037/96  
; FILING DATE: No. 6476197ember 29, 1996  
; APPLICATION NUMBER: JP 20,906/97  
; FILING DATE: January 21, 1997  
; APPLICATION NUMBER: JP 10,053,503  
; FILING DATE: No. 6476197ember 14, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: YAMAMOTO=15  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-982-285-4

Query Match 99.9%; Score 811; DB 4; Length 157;  
Best Local Similarity 99.4%; Pred. No. 3.8e-88;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

[illegible]

## RESULT 2

```

US-09-700-609-1
; Sequence 1, Application US/09700609
; Patent No. 6582689
; GENERAL INFORMATION:
; APPLICANT: Johnson, Randall K
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: P50777
; CURRENT APPLICATION NUMBER: US/09/700,609
; CURRENT FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/086,560
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Human
US-09-700-609-1

```

	Query Match	99.9%	Score 811;	DB 4;	Length 157;
	Best Local Similarity	99.4%;	Pred. No. 3.8e-88;		
	Matches 156;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	YFGKLESLVIRNLNDQVLFDIOGNRPLFEDMTDSDCRDNAPTIIISMYKDSQPRGM	60		
Db	1	YFGKLESLVIRNLNDQVLFDIOGNRPLFEDMTDSDCRDNAPTIIISMYKDSQPRGM	60		
Qy	61	AVTISVACEKISLSCENKIISFKEMNPPDNKTKSDIIFQFSVPGHNDKQMFESSY	120		
Db	61	AVTISVACEKISLSCENKIISFKEMNPPDNKTKSDIIFQFSVPGHNDKQMFESSY	120		
Qy	121	EGYFLACEKERDLFKLILKKEDELGDRSIMPTVQNE	157		
Db	121	EGYFLACEKERDLFKLILKKEDELGDRSIMPTVQNE	157		

RESULT 3

```

RESULTS 3
US-09-398-412B-7
; Sequence 7, Application US/09398412B
; Patent No. 6680380
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related reage
; TITLE OF INVENTION: method
; FILE REFERENCE: DX0904K
; CURRENT APPLICATION NUMBER: US/09/398,412B
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: US 60/100948
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-398-412B-7
Query Match 99.9%; Score 811; DB 4; Length 158;

```

	Best Local Similarity	29.4%	Pred. No. 3.8e-88;	Matches 156;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0
QY	1	YFGKLESLSVIRNLNDQVLFI	DQGNRPLFEDMTDSDCRDNAPRTIIFI	SMYKDSQPRGM	60							
Db	2	YFGKLESLSVIRNLNDQVLFI	DQGNRPLFEDMTDSDCRDNAPRTIIFI	SMYKDSQPRGM	61							
QY	61	AVTISVKCEKISXLSCENKI	LIISKEMNPPNIIKDTKSDI	IFORSVGHCHNKMQFESSY	120							
Db	62	AVTISVKCEKISLTSCENKI	LIISKEMNPPNIIKDTKSDI	IFQRSVGHCHNKMQFESSY	121							
QY	121	EGYFLACEKERDILFKLILK	KEDELGDRSIMFTVQNE	157								
Db	122	EGYFLACEKERDILFKLILK	KEDELGDRSIMFTVQNE	158								

## RESULT 4

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

	Query Match	99.8%	Score 810	DB 2	Length 157
	Best Local Similarity	100.0%	Prod. No. 4.9e-08		
	Matches 157	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	YFGKLEKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTFIITISMYKQSQRGM	60		
Db	1	YFGKLEKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTFIITISMYKQSQRGM	60		
Qy	61	AVTISVKEKISLXSCENKIIISFKEMPPDNIKOTKSDIIFFQRSVPGHDKNMQPESSSY	120		
Db	61	AVTISVKEKISLXSCENKIIISFKEMPPDNIKOTKSDIIFFQRSVPGHDKNMQPESSSY	120		

```
QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157

RESULT 5
US-08-896-501A-4
; Sequence 4, Application US/08896501A
; Patent No. 5891663
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896,501A
; FILING DATE: 18-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 213,267/1996
; FILING DATE: 25-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 31,474/1997
; FILING DATE: 31-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TANIMOTO=3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-896-501A-4

Query Match 99.8%; Score 810; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDSCRDNAPRTTIFIIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDSCRDNAPRTTIFIIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISXLSNCKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKMKQFESSY 120
Db 61 AVTISVKCEKISXLSNCKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKMKQFESSY 120

QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157

RESULT 6
US-08-884-324-1
; Sequence 1, Application US/08884324
; Patent No. 6060283
```

```
; GENERAL INFORMATION:
; APPLICANT: Takanori OKURA
; APPLICANT: Kakuji TORIGOE
; APPLICANT: Masahi KURIMOTO
; TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
; OF INDUCING THE PRODUCTION OF INTERFERON-
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/884,324
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 185,305/96
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: OKURA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-884-324-1

Query Match 99.8%; Score 810; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDSCRDNAPRTTIFIIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDSCRDNAPRTTIFIIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISXLSNCKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKMKQFESSY 120
Db 61 AVTISVKCEKISXLSNCKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKMKQFESSY 120

QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157

RESULT 7
US-08-996-338-26
; Sequence 26, Application US/08996338
; Patent No. 6087116
; GENERAL INFORMATION:
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: OKURA, Takanori
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
```

```
;
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,338
; FILING DATE: 22-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 74,697/1997
; FILING DATE: 12-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 215,488/1997
; FILING DATE: 28-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 291,837/1997
; FILING DATE: 09-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TORIGOE=3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-996-338-26

Query Match 99.8%; Score 810; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISXLSKENKIISFKEMNPPDNIKDTSDIIFQRSVPVGHNDKMQFESSY 120
DB 61 AVTISVKCEKISXLSKENKIISFKEMNPPDNIKDTSDIIFQRSVPVGHNDKMQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 8
US-08-558-818-1
; Sequence 1, Application US/08558818
; Patent No. 6197297
; GENERAL INFORMATION:
; APPLICANT: NAME: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
; APPLICANT: KENKYUJO
; APPLICANT: KUNIKATA, Toshio
; APPLICANT: TANIGUCHI, Mutsuko
; APPLICANT: KOHNO, Keizo
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,338
; FILING DATE: 22-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 74,697/1997
; FILING DATE: 12-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 215,488/1997
; FILING DATE: 28-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 291,837/1997
; FILING DATE: 09-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TORIGOE=3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-996-338-26

Query Match 99.8%; Score 810; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISXLSKENKIISFKEMNPPDNIKDTSDIIFQRSVPVGHNDKMQFESSY 120
DB 61 AVTISVKCEKISXLSKENKIISFKEMNPPDNIKDTSDIIFQRSVPVGHNDKMQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 9
US-08-974-469A-1
; Sequence 1, Application US/08974469A
; Patent No. 6207641
; GENERAL INFORMATION:
; APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
; APPLICANT: KENKYUJO
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: FUKUDA, Shigeharu
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: AGENT FOR SUSCEPTIVE DISEASE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect Version 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,469A
; FILING DATE:
; CLASSIFICATION:
```

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect Version 5.0
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: FELICI=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/558,818
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: JP 58,240/95
; PRIOR APPLICATION DATA: February 23, 1995
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-558-818-1

Query Match 99.8%; Score 810; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISXLSKENKIISFKEMNPPDNIKDTSDIIFQRSVPVGHNDKMQFESSY 120
DB 61 AVTISVKCEKISXLSKENKIISFKEMNPPDNIKDTSDIIFQRSVPVGHNDKMQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 9
US-08-974-469A-1
; Sequence 1, Application US/08974469A
; Patent No. 6207641
; GENERAL INFORMATION:
; APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
; APPLICANT: KENKYUJO
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: FUKUDA, Shigeharu
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: AGENT FOR SUSCEPTIVE DISEASE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect Version 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,469A
; FILING DATE:
; CLASSIFICATION:
```

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,879
; FILING DATE: March 10, 1995
; APPLICATION NUMBER: JP 78,357/95
; FILING DATE: September 29, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TORIGOE=1A
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-974-469A-1

Query Match 99.8%; Score 810; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFDIQGNRPLFEDMTSDCDRDNAPRTTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFDIQGNRPLFEDMTSDCDRDNAPRTTIFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISXLSKENKIISFKENPPDNIKDTKSDIIFQRSVPGHNDKMQFESSY 120
Db 61 AVTISVKCEKISXLSKENKIISFKENPPDNIKDTKSDIIFQRSVPGHNDKMQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 10
US-08-832-180-1
; Sequence 1, Application US/08832180
; Patent No. 6214584
; GENERAL INFORMATION:
; APPLICANT: KASUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
; APPLICANT: KENKYUO
; APPLICANT: USHIO, Shimpel
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: OKAMURA, Haruki
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: INTERFERON- PRODUCTION INDUCING
; TITLE OF INVENTION: POLYPEPTIDE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect Version 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/832,180
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/559,191
; FILING DATE:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,879
; FILING DATE: March 10, 1995
; APPLICATION NUMBER: JP 78,357/95
; FILING DATE: September 29, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TORIGOE=1A
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-974-469A-1

Query Match 99.8%; Score 810; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFDIQGNRPLFEDMTSDCDRDNAPRTTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFDIQGNRPLFEDMTSDCDRDNAPRTTIFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISXLSKENKIISFKENPPDNIKDTKSDIIFQRSVPGHNDKMQFESSY 120
Db 61 AVTISVKCEKISXLSKENKIISFKENPPDNIKDTKSDIIFQRSVPGHNDKMQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 11
US-08-832-198-6
; Sequence 6, Application US/08832198
; Patent No. 6242255
; GENERAL INFORMATION:
; APPLICANT: AKITA, Kenji
; APPLICANT: NUKADA, Yoshiyuki
; APPLICANT: FUJII, Mitsukiyo
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/832,198
; FILING DATE: 08-APR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/721,018
; FILING DATE: 25-SEP-1996
; APPLICATION NUMBER: JP 95-270725
; FILING DATE: 26-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 96-067434
```

```
;
; FILING DATE: 29-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP not yet received
; FILING DATE: 20-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: AKITA-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: "Xaa" in position 73 is either
; OTHER INFORMATION: 'ile' or 'thr'
;
US-08-832-198-6

Query Match          99.8%; Score 810; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
QY 61 AVTISVCKEKLXSLSCENKLIISFKEMNPPDNIKTKSDIIFQSVPGHDNKMQPESSSY 120
Db 61 AVTISVCKEKLXSLSCENKLIISFKEMNPPDNIKTKSDIIFQSVPGHDNKMQPESSSY 120
QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157

RESULT 12
US-09-819-902-6
; Sequence 6, Application US/09819902
; Patent No. 6403079
; GENERAL INFORMATION:
; APPLICANT: AKITA, Kenji
; NUKADA, Yoshiyuki
; FUJII, Mitsujiyo
; TANIMOTO, Tadao
; KURIMOTO, Masashi
;
; TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
;
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/819,902
; FILING DATE: 29-Mar-2001
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/832,798
; FILING DATE: 25-SEP-1996
; APPLICATION NUMBER: JP 95-270725
```

```
;
; FILING DATE: 26-SEP-1995
; APPLICATION NUMBER: JP 96-067434
; FILING DATE: 29-FEB-1996
; APPLICATION NUMBER: JP not yet received
; FILING DATE: 20-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: AKITA-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: "Xaa" in position 73 is either
; OTHER INFORMATION: 'ile' or 'thr'
;
US-09-819-902-6

Query Match          99.8%; Score 810; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
QY 61 AVTISVCKEKLXSLSCENKLIISFKEMNPPDNIKTKSDIIFQSVPGHDNKMQPESSSY 120
Db 61 AVTISVCKEKLXSLSCENKLIISFKEMNPPDNIKTKSDIIFQSVPGHDNKMQPESSSY 120
QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157

RESULT 13
US-09-752-510-6
; Sequence 6, Application US/09752510
; Patent No. 6441138
; GENERAL INFORMATION:
; APPLICANT: AKITA, Kenji
; NUKADA, Yoshiyuki
; FUJII, Mitsujiyo
; TANIMOTO, Tadao
; KURIMOTO, Masashi
;
; TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
;
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/752,510
; FILING DATE: 03-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/721,018
; FILING DATE: <Unknown>
```

APPLICATION NUMBER: JP 96-067434  
FILING DATE: 29-FEB-1996  
APPLICATION NUMBER: JP not yet received  
FILING DATE: 20-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: AKITA-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 157 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
OTHER INFORMATION: "Xaa" in position 73 is either  
'ile' or 'Thr'  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-752-510-6

Query Match 99.8%; Score 810; DB 4; Length 157;  
Best Local Similarity 100.0%; Pred. No. 4.9e-88;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
QY 61 AVTISVCKEKISXLSKCNKIISFKEMNPPDNIKDTSDIFFQRSVFGHDNKMQFESSY 120  
Db 61 AVTISVCKEKISXLSKCNKIISFKEMNPPDNIKDTSDIFFQRSVFGHDNKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157

RESULT 14  
US-09-711-899-1  
Sequence 1, Application US/09711899  
Patent No. 6509449  
GENERAL INFORMATION:  
APPLICANT: <Unknown>  
TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE  
WHICH INDUCES INTERFERON- PRODUCTION  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Browdy and Neimark  
STREET: 419 Seventh Street N.W. Ste. 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect Version 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/711,899  
FILING DATE: 13-No. 6509449-2000  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/588,818  
FILING DATE: 2000-11-15  
ATTORNEY/AGENT INFORMATION:  
NAME: Browdy, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: FELICI=1

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 157 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-711-899-1  
Query Match 99.8%; Score 810; DB 4; Length 157;  
Best Local Similarity 100.0%; Pred. No. 4.9e-88;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
QY 61 AVTISVCKEKISXLSKCNKIISFKEMNPPDNIKDTSDIFFQRSVFGHDNKMQFESSY 120  
Db 61 AVTISVCKEKISXLSKCNKIISFKEMNPPDNIKDTSDIFFQRSVFGHDNKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157  
RESULT 15  
US-09-556-972-26  
Sequence 26, Application US/09556972  
Patent No. 6559298  
GENERAL INFORMATION:  
APPLICANT: TORIGOE, Kakuji  
OKURA, Takanori  
KURIMOTO, Masashi  
TITLE OF INVENTION: POLYPEPTIDES  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/556,972  
FILING DATE: 24-Apr-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/996,338  
FILING DATE: 22-DEC-1997  
APPLICATION NUMBER: JP 74,697/1997  
FILING DATE: 12-MAR-1997  
APPLICATION NUMBER: JP 215,488/1997  
FILING DATE: 28-JUL-1997  
APPLICATION NUMBER: JP 291,837/1997  
FILING DATE: 09-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: TORIGOE=3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 157

```
;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-556-972-26

Query Match      99.8%; Score 810; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60
Db      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60

QY      61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQSVPGHDNKMQFESSY 120
Db      61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQSVPGHDNKMQFESSY 120

QY      121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db      121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
```

Search completed: August 19, 2004, 13:37:15  
Job time : 20 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2004, 13:35:10 ; Search time 46 Seconds  
(without alignments)  
1072.566 Million cell updates/sec

Title: US-09-716-356A-6

Perfect score: 812

Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKKEDELGDRSIMFTVQNEED 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1295152 seqs, 314255058 residues

Total number of hits satisfying chosen parameters: 1295152

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	811	99.9	157	9	US-09-775-046-9
2	811	99.9	157	10	US-09-030-061-6
3	811	99.9	157	12	US-10-247-703-65
4	811	99.9	157	12	US-10-247-703-71
5	811	99.9	157	13	US-10-100-057-6
6	811	99.9	157	13	US-10-094-153-2
7	811	99.9	157	14	US-10-260-576-4
8	811	99.9	157	14	US-10-297-136-1
9	811	99.9	157	14	US-10-311-491-3
10	811	99.9	157	15	US-10-397-786A-3
11	811	99.9	157	16	US-10-280-609-1
12	811	99.9	157	16	US-10-646-308-14
13	811	99.9	158	12	US-10-695-195-7
14	811	99.9	158	16	US-10-694-978-7
15	811	99.9	177	12	US-10-247-703-69

16	811	99.9	193	9	US-09-798-075-1	Sequence 1, Appli
17	811	99.9	193	9	US-09-770-528-8	Sequence 8, Appli
18	811	99.9	193	14	US-10-311-491-1	Sequence 1, Appli
19	811	99.9	193	16	US-10-679-201-5	Sequence 5, Appli
20	811	99.9	233	14	US-10-311-491-10	Sequence 10, Appli
21	810	99.8	157	8	US-08-996-140-1	Sequence 1, Appli
22	810	99.8	157	9	US-09-924-099-21	Sequence 21, Appli
23	810	99.8	157	14	US-10-327-069-1	Sequence 1, Appli
24	810	99.8	157	14	US-10-349-023-26	Sequence 26, Appli
25	810	99.8	193	16	US-10-646-308-13	Sequence 13, Appli
26	807	99.4	157	13	US-10-094-153-10	Sequence 10, Appli
27	807	99.4	193	13	US-10-094-153-9	Sequence 9, Appli
28	805	99.1	157	13	US-10-094-153-6	Sequence 6, Appli
29	805	99.1	157	13	US-10-094-153-7	Sequence 7, Appli
30	805	99.1	193	13	US-10-094-153-3	Sequence 3, Appli
31	805	99.1	193	13	US-10-094-153-4	Sequence 4, Appli
32	803	98.9	157	14	US-10-105-080-10	Sequence 10, Appli
33	803	98.9	193	14	US-10-105-080-4	Sequence 4, Appli
34	801	98.6	157	10	US-09-030-061-20	Sequence 4, Appli
35	801	98.6	157	13	US-10-100-057-20	Sequence 20, Appli
36	801	98.6	157	14	US-10-260-576-6	Sequence 6, Appli
37	799	98.4	157	12	US-10-247-703-77	Sequence 7, Appli
38	799	98.4	157	13	US-10-094-153-8	Sequence 8, Appli
39	799	98.4	193	13	US-10-094-153-5	Sequence 5, Appli
40	798	98.3	157	12	US-10-247-703-72	Sequence 72, Appli
41	795.5	98.0	156	15	US-10-414-774-1	Sequence 1, Appli
42	795	97.9	157	12	US-10-247-703-74	Sequence 74, Appli
43	792	97.5	157	12	US-10-247-703-75	Sequence 75, Appli
44	791	97.4	157	10	US-09-030-061-21	Sequence 21, Appli
45	791	97.4	157	10	US-09-030-061-22	Sequence 22, Appli

## ALIGNMENTS

RESULT 1  
US-09-775-046-9  
; Sequence 9, Application US/09775046  
; Patent No. US20020102234A1  
; GENERAL INFORMATION:  
; APPLICANT: Debets, Johannes Eduard Maria Antonius  
; APPLICANT: Timans, Jacqueline C.  
; APPLICANT: Bazan, J. Fernando  
; APPLICANT: Kastelein, Robert A.  
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RECEPTORS; RELATED REAGENTS AND METHODS  
; FILE REFERENCE: DX01073K  
; CURRENT APPLICATION NUMBER: US/09/775,046  
; PRIOR FILING DATE: 2001-02-01  
; PRIOR APPLICATION NUMBER: 60/179,638  
; PRIOR FILING DATE: 2000-02-02  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-775-046-9

Query Match	99.9%;	Score 811;	DB 9;	Length 157;
Best Local Similarity	99.4%;	Pred. No. 3.1e-81;		
Matches 156;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	YFGKLESKLSVIRNLNDQVLFDIQGNRPLFEDMTSDCRDNAPRTFIISMVKDSQPRGM	60	
Db	1	YFGKLESKLSVIRNLNDQVLFDIQGNRPLFEDMTSDCRDNAPRTFIISMVKDSQPRGM	60	
QY	61	AVTISYKCBKISXLSKCNKIISFKENMPDNIKDTKSDIIFQORSVPGHDKNMQFESSY	120	
Db	61	AVTISYKCBKISXLSKCNKIISFKENMPDNIKDTKSDIIFQORSVPGHDKNMQFESSY	120	
QY	121	EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED	157	
Db	121	EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED	157	

```

; APPLICANT: Snyder, Linda A
; TITLE OF INVENTION: NUCLEIC ACID VACCINES USING TUMOR ANTIGEN ENCODING NUCLEIC ACIDS
; FILE OF INVENTION: CYTOKINE ADJUVANT ENCODING NUCLEIC ACID
; FILE REFERENCE: CEN310
; CURRENT APPLICATION NUMBER: US/10/247,703
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 65
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-247-703-65

Query Match 99.9%; Score 811; DB 12; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNAPRTIFIISMVKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNAPRTIFIISMVKDSQPRGM 60
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMKQFESSY 120
Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 4
US-10-247-703-71
; Sequence 71, Application US/10247703
; Publication No. US20030063597A1
; GENERAL INFORMATION:
; APPLICANT: Branigan, Patrick
; APPLICANT: Goletz, Theresa J
; APPLICANT: Knight, David M
; APPLICANT: McCarthy, Stephen G
; APPLICANT: Scallion, Bernard J
; APPLICANT: Snyder, Linda A
; TITLE OF INVENTION: NUCLEIC ACID VACCINES USING TUMOR ANTIGEN ENCODING NUCLEIC ACIDS
; FILE OF INVENTION: CYTOKINE ADJUVANT ENCODING NUCLEIC ACID
; FILE REFERENCE: CEN310
; CURRENT APPLICATION NUMBER: US/10/247,703
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 71
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-247-703-71

Query Match 99.9%; Score 811; DB 12; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNAPRTIFIISMVKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNAPRTIFIISMVKDSQPRGM 60
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMKQFESSY 120
Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

US-09-030-061-6
; Sequence 6, Application US/09030061
; Publication No. US20030095946A1
; GENERAL INFORMATION:
; APPLICANT: GILLISPIE, Matthew Todd
; APPLICANT: HORWOOD, Nicole Joy
; APPLICANT: UDAGAWA, No. US20030095946A1uyuki
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,061
; FILING DATE: 25-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 55,468/1997
; FILING DATE: 25-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: GILLISPIE-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-030-061-6

Query Match 99.9%; Score 811; DB 10; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNAPRTIFIISMVKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNAPRTIFIISMVKDSQPRGM 60
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMKQFESSY 120
Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 3
US-10-247-703-65
; Sequence 65, Application US/10247703
; Publication No. US20030063597A1
; GENERAL INFORMATION:
; APPLICANT: Branigan, Patrick
; APPLICANT: Goletz, Theresa J
; APPLICANT: Knight, David M
; APPLICANT: McCarthy, Stephen G
; APPLICANT: Scallion, Bernard J
```

```
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 5
US-10-100-057-6
; Sequence 6, Application US/10100057
; Publication No. US20020150555A1
; GENERAL INFORMATION:
; APPLICANT: GILLISPIE, Matthew Todd
; HORWOOD, Nicole Joy
; UDAGAWA, No. US20020150555A1uyuki
; KURIMOTO, Masashi
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/100,057
; FILING DATE: 19-Mar-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,061
; FILING DATE: 25-FEB-1998
; APPLICATION NUMBER: JP 55,468/1997
; FILING DATE: 25-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: GILLISPIE=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-100-057-6
Query Match 99.9%; Score 811; DB 13; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDKTSIIFFQRSVPGHDKMKQFESSY 120
Db 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDKTSIIFFQRSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 7
US-10-260-576-4
; Sequence 4, Application US/10260576
; Publication No. US20030092130A1
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, Kozo
; OKAMOTO, Iwao
; KURIMOTO, Masashi
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 7th Street N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/260,576
; FILING DATE: 01-Oct-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/982,285
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 333,037/96
; FILING DATE: No. US20030092130A1ember 29, 1996
; APPLICATION NUMBER: JP 20,806/97
; FILING DATE: January 21, 1997
; APPLICATION NUMBER: JP 10,053,503
; FILING DATE: No. US20030092130A1ember 14, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: YAMAMOTO=15
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; APPLICANT: Dinarello, Charles
```

```

; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 157 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-260-576-4

Query Match          99.9%; Score 811; DB 14; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNAPRTIFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNAPRTIFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKMQFESSY 120
DB 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKMQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 8
US-10-297-136-1
; Sequence 1, Application US/10297136
; Publication No. US20030113292A1
; GENERAL INFORMATION:
; APPLICANT: ESSER, KLAUS M.
; APPLICANT: ROSENBERG, MARTIN
; APPLICANT: TAL-SINGER, RUTH
; APPLICANT: WOODNUTT, GARY
; APPLICANT: CHISARI, FRANCIS V.
; APPLICANT: DILLON, SUSAN B.
; TITLE OF INVENTION: Methods of Treating Viral Diseases with
; FILE REFERENCE: P51144
; CURRENT APPLICATION NUMBER: US/10/297,136
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: PCT/US01/17924
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/208,869
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-297-136-1

Query Match          99.9%; Score 811; DB 14; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNAPRTIFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNAPRTIFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKMQFESSY 120
DB 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKMQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

US-10-312-491-3
; Sequence 1, Application US/10311491
; Publication No. US20030143198A1
; GENERAL INFORMATION:
; APPLICANT: JOHANSON, KYUNG O.
; APPLICANT: KIRKPATRICK, ROBERT B.
; APPLICANT: SHATZMAN, ALLAN R.
; APPLICANT: HO, YEN SEN
; APPLICANT: MCDEVITT, DAMIEN
; TITLE OF INVENTION: Method for Preparing a Physiologically
; FILE REFERENCE: P51137
; CURRENT APPLICATION NUMBER: US/10/311,491
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/US01/18804
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/211,832
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/224,128
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/264,923
; PRIOR FILING DATE: 2001-01-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-311-491-3

Query Match          99.9%; Score 811; DB 14; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNAPRTIFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNAPRTIFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKMQFESSY 120
DB 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKMQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

US-10-397-786A-3
; Sequence 3, Application US/10397786A
; Publication No. US20040018195A1
; GENERAL INFORMATION:
; APPLICANT: GRISWOLD, DONALD
; APPLICANT: LI, LI
; APPLICANT: LI, JIAN
; TITLE OF INVENTION: DIABETES DISEASE DERIVED PROTEINS, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN-0287
; CURRENT APPLICATION NUMBER: US/10/397,786A
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/367,902
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver 2.0
; SEQ ID NO 3
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-397-786A-3

Query Match          99.9%; Score 811; DB 15; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNAPRTIFIISMYKDSQPRGM 60

```

```

; Sequence 3, Application US/10311491
; Publication No. US20030143198A1
; GENERAL INFORMATION:
; APPLICANT: JOHANSON, KYUNG O.
; APPLICANT: KIRKPATRICK, ROBERT B.
; APPLICANT: SHATZMAN, ALLAN R.
; APPLICANT: HO, YEN SEN
; APPLICANT: MCDEVITT, DAMIEN
; TITLE OF INVENTION: Method for Preparing a Physiologically
; FILE REFERENCE: P51137
; CURRENT APPLICATION NUMBER: US/10/311,491
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/US01/18804
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/211,832
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/224,128
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/264,923
; PRIOR FILING DATE: 2001-01-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-311-491-3

Query Match          99.9%; Score 811; DB 14; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNAPRTIFIISMYKDSQPRGM 60

```

```

; Sequence 3, Application US/10397786A
; Publication No. US20040018195A1
; GENERAL INFORMATION:
; APPLICANT: GRISWOLD, DONALD
; APPLICANT: LI, LI
; APPLICANT: LI, JIAN
; TITLE OF INVENTION: DIABETES DISEASE DERIVED PROTEINS, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN-0287
; CURRENT APPLICATION NUMBER: US/10/397,786A
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/367,902
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver 2.0
; SEQ ID NO 3
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-397-786A-3

Query Match          99.9%; Score 811; DB 15; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNAPRTIFIISMYKDSQPRGM 60

```

```
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTTIIISMYKDSQPRGM 60
Qy 61 AVTISVKCEKISLSCENKIISFKEMPPDNKDKSDIIFQFORSVFGHDKMKQFESSY 120
Db 61 AVTISVKCEKISTLSCENKIISFKEMPPDNKDKSDIIFQFORSVFGHDKMKQFESSY 120
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 11
US-10-280-609-1
; Sequence 1, Application US/10280609
; Publication No. US20040023336A1
; GENERAL INFORMATION:
; APPLICANT: Heavner, George
; APPLICANT: McCarthy, Stephen G.
; TITLE OF INVENTION: IL-18 OR MUT-IL-18R PROTEINS, ANTIBODIES, COMPOSITIONS,
; FILE REFERENCE: CEN0321
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/10/280,609
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 60/335,880
; PRIOR FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver 3.1
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-280-609-1

Query Match 99.9%; Score 811; DB 16; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTTIIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTTIIISMYKDSQPRGM 60
Qy 61 AVTISVKCEKISLSCENKIISFKEMPPDNKDKSDIIFQFORSVFGHDKMKQFESSY 120
Db 61 AVTISVKCEKISTLSCENKIISFKEMPPDNKDKSDIIFQFORSVFGHDKMKQFESSY 120
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 12
US-10-646-308-14
; Sequence 14, Application US/10646308
; Publication No. US20040136992A1
; GENERAL INFORMATION:
; APPLICANT: BURTON, Paul B. J.
; APPLICANT: DEISHER, Theresa A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DISEASE
; FILE REFERENCE: 3432-B
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US/10/646,308
; PRIOR FILING DATE: 2003-08-12
; PRIOR APPLICATION NUMBER: 60/406,418
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 14
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```
US-10-646-308-14

Query Match 99.9%; Score 811; DB 16; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTTIIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTTIIISMYKDSQPRGM 60
Qy 61 AVTISVKCEKISLSCENKIISFKEMPPDNKDKSDIIFQFORSVFGHDKMKQFESSY 120
Db 61 AVTISVKCEKISTLSCENKIISFKEMPPDNKDKSDIIFQFORSVFGHDKMKQFESSY 120
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 13
US-10-695-195-7
; Sequence 7, Application US/10695195
; Publication No. US20040068099A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/695,195
; FILING DATE: 27-Oct-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/398,412
; FILING DATE: 17-Sep-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DXO904K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-695-195-7

Query Match 99.9%; Score 811; DB 12; Length 158;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTTIIISMYKDSQPRGM 60
Db 2 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTTIIISMYKDSQPRGM 61
Qy 61 AVTISVKCEKISLSCENKIISFKEMPPDNKDKSDIIFQFORSVFGHDKMKQFESSY 120
```

Db 62 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKKQFESSY 121  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 122 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 158

## RESULT 14

US-10-694-978-7  
; Sequence 7, Application US/10694978  
; Publication No. US20040087766A1  
; GENERAL INFORMATION:  
; APPLICANT: Timans, Jacqueline C.  
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/694,978  
; FILING DATE: 27-Oct-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/398,412  
; FILING DATE: 17-Sep-1999  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Egwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0904K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650)852-9196  
; TELEFAX: (650)496-1200  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 158 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-10-694-978-7

Query Match 99.9%; Score 811; DB 16; Length 158;  
Best Local Similarity 99.4%; Pred. No. 3.1e-81;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNDNAPRTIFIISMVKDSQPRGM 60  
Db 2 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNDNAPRTIFIISMVKDSQPRGM 61  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKKQFESSY 120  
Db 62 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKKQFESSY 121  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 122 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 158

## RESULT 15

US-10-247-703-69  
; Sequence 69, Application US/10247703  
; Publication No. US20030063597A1  
; GENERAL INFORMATION:

; APPLICANT: Branigan, Patrick  
; APPLICANT: Goletz, Theresa J  
; APPLICANT: Knight, David M  
; APPLICANT: McCarthy, Stephen G  
; APPLICANT: Scallion, Bernard J  
; APPLICANT: Snyder, Linda A  
; TITLE OF INVENTION: CYTOKINE ADJUVANT USING TUMOR ANTIGEN ENCODING NUCLEIC ACID  
; FILE REFERENCE: CEN310  
; CURRENT APPLICATION NUMBER: US/10/247,703  
; CURRENT FILING DATE: 2002-09-20  
; PRIOR APPLICATION NUMBER: 60/328,371  
; PRIOR FILING DATE: 2001-10-10  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO: 69  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-247-703-69

Query Match 99.9%; Score 811; DB 12; Length 177;  
Best Local Similarity 99.4%; Pred. No. 3.6e-81;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNDNAPRTIFIISMVKDSQPRGM 60  
Db 21 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNDNAPRTIFIISMVKDSQPRGM 80  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKKQFESSY 120  
Db 81 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKKQFESSY 140  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 141 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 177

Search completed: August 19, 2004, 13:38:12  
Job time : 46 secs